

FIGURE 1

ACTGCACCTCGTTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCGGGCCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCG
CAGCGCTACCCGCATGCGCTGCGCCGGGCCGGCTGGGCTCTGCGCTTCTGCTG
CTGCTGCCGCCCGCGCCGGAGGCCAAAGAGCGACGCCCTGCCACCGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGGATGGTGACACCGAAAGAAGAACTTGGCGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCAGTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCGACTGAAGAGCGAATATCTGACTTATTCGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCAGGAACCTACGGTCCCAGTGTCTGCATGC
CAGGGCGGATCCCAGAGGCCCTGCGAGCGGAATGCCACTGCAGCGAGATGGGAGCAGACA
GGGCGACGGGCTCTGCCGGTGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCGGAACGAGACCCACAGCATCTGCACAGCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCTGTGGATGTGGACGGAGTGTGCGGCCAGCGCCCTCCCTGCAGCGCTG
CCCAGTTCTGTAAGAACCCAACGGCTCTACAGTGCAGAGACTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGGTGATCTCTGGCTACGCAGGGAGCA
CGGACAGTGTGCAAGATGTGGACAGTGCTCACTAGCAGAAAAAAACCTGTGAGGAAAACG
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTCTGACGGCTTCGAAGAAAACG
GAAGATGCGCTGTGCGCCGCGAGGGCTGAAGGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACCTGTATGTGCCGACTTACCTTAAATTATTCAAGAGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCTGCACTGGACAGCGCGGGGAGGGCTG
CTGCTCTAAGGGTGTCTTGTGCTTAAACAGCTGCAATTCTGGTTGTTCTTA
AACAGACTGTATATTTGATACTGTTGTAATAAAATTGACCATTTGAGGTTAATCAGG
AGGAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTGCACCTGCAAGAAGC
TTGGCCGCATGGCCAACCTGTTATTGCACTTATAATGGTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTTCACTGCATTCTAGTTGTGGTTGTCAAACACT
ATCAATGTATCTTATCATGTCTGGATGGAAATTAACTGGCGCAGCACCATGGCTGAAAT
AACCTCTGAAGAGGAACCTGGTAGGTACCTCTGAGGGGAAAGAACCCAGCTGGAAATG
TGTGTCAAGTGTGGAAAGTCCCAAGGCTCCCCAGCAGGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPFRRAALGLLPLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCILACQGGSQRPCSG
NGHCSDGDSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSIC^TACDESCKTCGLTNRDCGECEVGWVLDE
GACVDVDCEAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNC^KECISGYAREHGQCADVDEC^LA^EKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCAACTGCACCTCGTTCTATGATTGAAATCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGTCCGCCAGGCCGGAGGCAGCCGCCAGCGCTCTAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGGAGGAGTTTCGGGAGCTGGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
CTGGCCCGCGCAGCTGGCTCTGGAGCATCTCCCTGCTGCGCTGGCACTGCCGGCGGAGGC
CGGGCCGCCAGGAGGAGCTGACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA
TAGGATTGAGAAAGATATCTGATTGTTTCAAGAGGGAAAATGCCACCTTTAACATGAT
TTCAGAAAAGGCCAACAGAGAATGCCAGTATCTGTCATTAATCCATTCCATGAAATTTCAC
CTGGCAAGCTGAGGGCAGGCAAGAACATCTGTCATGAAATTCTGCTCTGGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGCCCTCTGGAAACAGTGCCCTCACAGGCA
TCAGTCTGTCACCTGGTTTCCATGTTCTGGAAAACAGGATGGGGCGCAGCTTGAAGT
GGATGTTGATTGTTATGAAATTCTGAAACAGGCAACACCATTCTCAAACACTCAAATGCTATCT
TCTTTAAACATGTCACAAAGCTGACTGCCAGGGTGGCGAAATGGAGGCTTGTAA
GAAAGACGCATCTGCGAGTGTCTGATGGTTTCAAGGCCACTACTGTGAGAAAGCCCTTG
TACCCCCAGCTGATGTAATGGTGGACTTGTGACTCTGGATCTGCACTTGCCCACCTG
GATTCTATGGGACTGCAACTGTCACAAAGCCTAACACTGCTCACCAACTCTGCTTAA
TGGAGGGACCTGTTTCAACCCCTGAAATGGGTTAAATGGTAAAGCCTTGGCAACTGTT
CCAAAGGTTACCGAGGGAGACCTCTGTTCAAGGCCCTGCGAGCTGGCTGTGGTCACAT
GGAACCTGCCATGAACCCAAACATGTCAGAAGGGTGGCATGGAAAGACACTGCAA
TAAAAGGTACGAAGGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCCAGC
ACACCCCTCACTTAAAAAGGCCAGGGAGGGGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACCTTTAAGTACACCAAGTTCATAGCCTTGTAACTCTTCA
TGTGTTGAATGTTCAAAATAATGTTCACTTAACTTAAGAATACTGGCTGAAATTATTAGCT
TCATTATAAAACTACTGAGCTGATATTCTCTCTTAAAGTTTCTAAGTACGTCGTTAG
CATGATGGTATGATTTCTCTTCACTGTTGGGACAGATTATATTATGTCAAATG
TCAGGTTAAAATTTCAGTGTGAGITGGCAGATATTCTAAATTACAATGCAATTATGGT
GTCTGGGGCAAGGGAAACATCAGAAAGCTTAAATTGGGAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTCAGTTAATGTTGAAGGTTACAGCATTTCAGATTTTATTGTCAGATATTAGAT
GTTGTTTACATTTTAAAAATTGCTCTTAAATTTTAAACTCTAACATACAATATATTGAC
TTACCAATTATCCAGAGATTCTGAGTATTAAAAAAAAAAATTACACTGTTGAGTGGCATTT
AAACAATATAATATATTCTAAACACAATGAAATAGGGAAATATAATGTTGAGTGAACCTTTG
TGGCTTCAAGCAATATAATTGTAACAAAACACGCTCTTACCTAATAAACATT
ACTGTTGTTGAGTATAAAATAAGGTGCTGCTTTAGTTTTGGAAAAAAA
AAAAAAAAAAAAAAAAGGGCGCCCGACTCTAGAGTCACCTGCAAGCTTGGC
GCCATGGCCAACCTGTTATTGCACTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQRMPAI PVNIHSMNFTWQAAGQABYFYEFLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEQECEISKCPQPCRNGKCIGKSCKCSKGYQGDLCSPKVC
EPGCGAHTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCGGCGGTCGCAGAGCCAGGAGGCCAGGAGGCCAGGAGGCCAGGCCAGCTGGG
CCCCAGCCCACACCTTCACCAAGGCCAGGAGCCACCATGTGGCAGTGTCCACTGGGGCTAC
TGCTGTGCTGCGCTGCGTGGCACTTGGCTCTGGGTGCCAGCAGGGCTGTGGGGCG
GAGCTAGCACCGGGCTGCAACCTGCCGGGATCCGGGAGCAGGGCTACTGCCAGGA
GCAGGACCTGTGCTGCCGCCGGCTGCCGAGACTGTGCCCTGCCATACCTGGGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGCCGCTGCCACCCCTTTTCCCGATCCAAGGATGTATGCACTGGAGGTCTATCTA
TCCAGTCTTGGGAACTGACTGGGAACTGTAAACCGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCAGACATGTCAAAGGCATCAACCCAGGGCAACTATGGCTGGCAGGCTGG
GAACCCACAGGCCCTCTGGGCTGACCCCTGGAATGAGGGCATTGCTACCGCCTGGCACCA
TCCGCCCATCTCCCGTCACTGAAACATGGCATGAAATTTATACTAGTGTGAACACCAGGGAG
GTGCTTCCCACAGGCCCTGGGCCCTGAGAAGTGGCCCAACCTGATTCATGACCTCTTGA
CCAAGGCAACTGTGCAGGCCCTGGGCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCATTCTCTGGGACACATGACGCCCTGTGCTGCCAGAACCTGCTGTGCTGTGAC
ACCCACAGCAGCAGGGCTGCCGCCGGCTCGATGGTGCCTGGTGGTCTCTGGCTCG
CCGAGGGTGGTGTGACCACTGCTACCCCTCTGGGGCTGTAACCGAGACAGGGCTGGCC
CTGGGCCCTGTATGATGACAGCCGAGCATGGTGGGGCAAGGCCAGGCCACTGCC
CACTGGCCCAACAGCTATGTTAAACAATGACATCTACCGGCTACTCTGTCTACGCC
CGGCTCCAACGACAAGGAGATCATGAAGGGAGCTGTGAGAATGGCCCTGTCCAAGGCC
TGGAGGTGATGAGGACTCTTCTCTATAACAGGGAGGATCTACAGGCCACAGCCAGTGA
CTTGGGAGGCCAGAGAGATACCCGGCATGGGACCCACTGAGTAAGATCACAGGATGGGG
AGAGGAGACCTGCGCAAGGACCTCAAAATCTGAGCTGCCCAACTCTGGGG
CAGGCCCTGGGGCGAGAGGGCCACTTCCGATCGTGGCCGGCTCAATGAGTGGCAGTCAG
AGCTTCTGCTGGGCTCTGGGCGTGGGATCGGGCATGGAGGACATGGGTCACTGAGGCTG
CGGGCACCCAGGCCCTGGGCGTGGGATCCAGGCTAAGGGCGGGAGAGGGCCCAATG
GGGCGGGTGCACCCAGCCTCGCCGACAGAGGCCGGGGCAGGCCAGGGCGCCAGGG
CCCCGGCGGGGTTCCGCTGACGCGAGGCCCGCCCTGGAGGCCGGCAGGGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGACGGGGCAGGGCTGGGAGAGGACACAGCTGCAG
ATCCCCAGGCCCTCTGGGCCCTTCAACAGACTACCAAAAGCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTAGACAGGGCTTGTCTCCG
TTGCCCCAGGTGGAGTGCAGTGGCCATCAGGGCTACTGTAACCTCCGACTCTGGGTTCA
AGTGACCCCTCCACCTCAGGCTCTCAAGTAGCTGGGACTACAGGTGACCCACACCTGGC
TAATTTTTGTATTTTTGTAAAGGGGGGCTCACTGTGTTGCCAGGCTGGTTCA
CCTGGGCTCAAGCGGTCCACCTGCCCTCCCAAGTGTGGGATTGCAAGGAGACT
ACTGCACCCAGGCCCTGATTTCTCAGATATTATTTCTTCACTGTGTTCA
AAAAACCAAAGTATTGATAAAAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYQCQEQLCCRGRADDC
ALPYLGAICYCSDLFCNRTVSDCCPFDWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTTGGACACATNACGCCGTCTTCCTTNGCCCCAGAACCTGCTGTCTTGACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGAACGTGCCCTGCAGGGAGAAGTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCTCCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCAACGGACTACTACGTGGCAAGAAGAACATCACCTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGACTCGGCCGTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCCACACTGGGTGTGGTGCCTCAGGCCACTGTGCCACTCCTCACAGACCTG
GCCCACTGGGAGCCTGCTGGTCTGGAGGCACATCTTAACGCAAGTCTGACCATGATGT
CTGCACCCCTGCCCCACCCCTGACCCCTCATGGCCCTCTCCAGGACTCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATCTCCACCCCTTAACCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAGGCTGAGATGAAGTGGACTGAGTAGAACTGG
GGACAAGAGTCGACGTGAGTCCCTGGAGCTCCAGAGATGGGCCTGGAGGCTGGAGGAA
GGGGCCAGGCCACATTCTGGGGCTCCCTGAATGGCAGCCTGAGCAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLLTDLAQWEPVLVPEAHPNASLTMYCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAGFSTLNPNVLRLFPQEAFPAHPYDLSQVWSVVSPAPSRSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCTCGAACCTCTCAGCGATGGGAGCCGCCCTGCCTGCCAACCTCACTCTG
GCTTACAGCTGCTGATTCTCTGCTGTCAAACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGGCGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCAGGGACGCCAACAAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGGGGTTCGCATCAAAGGGCTGAGAGTGGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATACGGCCCTCCAGAACGCCCGCACGAGG
GCTGGTTATGGCCTTCACGCCAGGGCGGGCCCGCAGGCTTCCGCAGGCCAGAAC
CAGCGCAGGGCCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGAGAACGAGCTTCGAGTTGTGGCTCGGCCAACCGCCGGACCAAGCGCACAC
GGCGGCCCAGAGCCCTCACGTAGTCTGGGAGGCAGGGCAGCAGCCCCCTGGGCCCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGGCCAGATCCCC
GAGGGAGGACCTGAGGCCCGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCCCTTCCCGAGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTGGATCTCCCTCAGTCTGCCAACGCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGAGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCAACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIKIVETDTFGSRVRIKGAESEKYICMNNKRGKLIGKPSGSKDCVFTIEIVLE
NNYTAFCQNRHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQQQLPFPNHAEKQKQFEF
VGSAPTRRTKRTTRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAAATTCTCCCTGTTGAATTTCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGAGTCTCTAGCTGGAGTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTCGTTTATTTTTCTTTCTTTCCCACATTGTATTTAT
TTCCGTACTTCAGAAATGGCCATACGACCAAAGATGGCCAGGCCATGGGCTTTTCT
GAAGCTTGGCTTATCATTCCTGGGCTCTACTCACAGGTGTCAAACTCTGGCCTGCC
CTAGTGTGCGCTGCAGGAACCTTGCTACTGTATGAGCGAAGCTTGACCTCAGTG
CCTCTGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAAACAAACCAATTAAATG
TGGATTCTCTGAGAACTGACAATGTACAGTCGGTCAACAGGTCTACCTGTATGGCAACC
AACTGGACGAATCCCCATGAACCTCCAAAGAATGTCAGAGTTCTCCATTGAGGAAAC
AAATTCAGGACCATTCAGGGCTGCTCTGGAGCTTGAAGAGCTGCACT
GGATGACAACCTCATATCCAGTGGGGTGGAAAGACGGGGCTTCCGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTTGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATCCGACATGGCTTCCAGAA
TCTCACAGGCTTGGAGCGCTTATGAGCAGGGAACTCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCGCCATCTCCAAGGAATTTCATGTAATTCGCTGTG
CACCCCTCTCCGATCTCCAGGTACGACTTGATCAGGCTCTATTGAGGACAACCAAGAT
AAACACCATCTTGTGACAGCTCTCAATCTGCTTAAGCTGGAAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTACTCAAGGGGTTTGTATACTCTCCAAACCTGAGCAGCTC
ACTGCTGGATAACCCCTGGTTTGTACTGAGTATTAAATGGGTACAGAATGGCTCAA
ATATATCCCTCATCTCAACGTCGGGTTTGTGCAAGGCTCTGAACAAGTCCGG
GGATGGGCTCAGGGAAATTAAATGAAATTGTTGCTCTGCCACAGGCCCGGGCTG
CCTCTCTCACCCTAGCCCCAGTACAGCTCTCCGACACTCAGCCTCCACCTCT
TCCAACCCTAGCAGAAAGCTACAGCCTCCAACCTCTACCATGAAACTTCCACGATT
CTGACTGGGATGGCAGAGAAAGGTGACCCACCTATTCTGCAAGGGATCCAGCTCT
CATTTGTGAATGATATTCTCAAGTCAGCTGGCTCTCTCTTCACTGTGATGGCATA
CAAACTCACATGGGTGAAATGGGCCACAGTTAGTAGGGGATCGTTCAGGAGGCATAG
TCAGCGGTGAGAAGCAACACTGAGCTGTTAACTTAGAGCCCCGATCCACCTCGGATT
TGTTTAGTGCCTGGATGTTTAACTACCGCGCGGTAGAAGACACCATTTGTTCAAGGGC
CACCACCATGCTCTCTATCTGAAACAACGGCAGAACACAGCTCCAGCCATGAGCAGCCA
CGTCCCACAGCATGGGCTCCCCCTTCTGCTGGCGGCTTGTGCGGGGCGCGTGTGATATT
GTGCTGGTGGCTTGCTCAGCGTCTTTGCTGGCATATGACACAAAAGGGGCGTACACCTC
CGAGAAGTGGAAATACAACCGGGCGGGCGAAAGATGATTATTGAGGAGCAGGACCAAGA
AGGACAACCTCATCTGGAGATGACAGAAACAGTTTCAGATGTCCTTAAATAACGAT
CAACTCTTAAAGGAGATTCTGAGACTCTGAGCCATTACACCCAAATGGGGGCTTAAATTA
CACAGACTGCCATATCCCAACACATGCCATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGCAAGCCAGAGGCCAGCGTTATGACAGGCGACAATTAGACTCTGAGAA
CACACTCGTGTGTCACATAAAGACACCGCAGATTACATTGATAAATGTTACACAGATG
TGTGCAATTGAAATACTCTGTAATTATAACGGTGACTATATAATGGGATTAAAAAGTG
CTATCTTCTATTCAAGTTAAATTACAAACAGTTGTAACTCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGaffFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLVLYLHNQNQINNAGFPAAELHNVQSVHTVYLYGNQLDEFPMNLPKNRVRLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAISSLKLLFLSKNHLSVPVGLPVPLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNNLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNCLRMLTOGVFDNLNSNLQOLTARNN
PWFCDCSIKWVTEWLKYI PSSLNVRGFMCGQPEQVRGMARVELNMNLLSCPTTPGPLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPTPPTSKLPTIPDWDRERVTPTPISERIQLSIHFVN
TSIQVSWLSLFTVMAYKLTVVKMGSVLGGIVQSERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLIAGLIGGAIVFVLUVV
LSVFCWHMHKKGRYTSQWKYNRGRKDYCEAGTKKDNSILEMTETSFQIVSLNNNDQLLG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRRHARTHPTQTALESCENKRADLVFIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLTKPDKSEVERAVKRMRLHSLTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHFCINIPGSYVCRKCKQGYILNSDQTTCRIQDLCAMEDHNCSEQLCVNPVGSFVCQCYSGYALAEKGRCRVADYCASENHGCEHECVNADGSYLCQCACHEGFALNPDEKTCTRINYCALNKGCEHECVNMEESYYCRCHRGYTLDPNGKTCRSRVDHCAQQDHGCEQQLCLNTEDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCEYSVNMDRSFAQCPCGHVLRSDGKTCALKLDSCALGDHGCEHSCVSSEDSFVCQCFCFGYLREDGKTCRKDVCAIDHGCEHICVNSSDSYTCECLEGFRLAEDGKRCRKDVCKSTHHGCEHICVNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVIDGSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNPFNSAKDMKAVAHMKYMGKGSMTGLALKHMFERSFTPKHLYAEDFSTMDEISEKLKGICEALEDSDGRQDSPAGELPKTVQQPTESEPVTINIQDLLSCNFVAVQHRYLFEEFDNLLRSTQKLSHSTKPGSPLEEKHDQCKCENLIMFQNLANEERVRKLTQRLEEMTQRMELAENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTGCAGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCAGGGCTGGCGCCCCCTGACTCCGTCGGTTTTGTTCTGGGCTGA
CATGATTCCCTCCCGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCTCGGGGCCAGCTGCAACTGCACTTGCCGCCAACCGGTTGCAG
CGGGTGGAGGGAGGGAAAGTGGTGTCCAGCGTGGTACACCTTGCAACGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTACTCC
ATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGTCTCCAGGAGAAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAAACAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTAAGTGTCCAGCTCCATCTGCCGTCTCCAGGGTGTGCCCTAT
GTGGGGCAACGTGACCCGTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCAAATACCA
GTGGGATCGGCAGCTCCATCCTTCAGACTTCTTGACCCAGCATTAGATGTCATCCGT
GGTCTTAAGCCTCACCAACCTTCTGCTTCCATGGCTGGAGTCTATGTCAGCAAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAGTGAGCACAGGGCCTGGAGCTG
AGTGGTGCTGGAGCTGTTGTTGACCTCTGGTGGACTGGGTTCTGGCTGGCTGGTCC
TCTTGACCCGGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCTGCCCTGGCCCAAGAGCTCAGACACAATCTCAAGAATGGACCT
TCCCTCTGTCACCTCCGACGAGCCCTCCGGCACCCATGGCCCTCCAGGCTGGTGCAT
TGACCCCAAGGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCTCAACCAATATCCCCATCCCTGGTGGGTTCTCTCTGGCTTGAGCCG
CATGGTGCTGCTGCTGTGATGGTGCCCTGGCCAGAGTCAGACTGGCTCTGGTAT**TGATGAC**
CCCACCACTCATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCTGAGTCATGGAAAGAGTCACACTCTGACCCCTAGTACTCTGCCCAACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAAGTCTCCAGG
CCCCCTGATCTGACCCACCCCTATCAACACCACCCCTGGCTCCACTCCAGCTCCAG
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGAGGAGATAGGAATCTC
TTATTAAAACATGAAATATGTGTTGTTCTTGCAAATTAAATAAGATACTAA
TGTGTTGATGAAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQ
WDRQLPSFQFFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLLEVSTGPGAA
VVAGAVVGTIVLGLLLAGLVLLYHRRGKALEEPANDIKEADIAAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQFISPIPGGVSSGLSR
MGAVPVPMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCCCACTGGGCCACGCCAATGAAACGCCCTCCGCTCTAGGGTTTCACTTTG
TTGAATTGTCCTATACTCAAATTGCCAACAGACACTTGCTCCAAATGCAAAATGTGA
AAATCGCAATGAACTGCAACAGACACTTGCTCCAAATGCAAAATGTGA
TTTGTGAAGATGATAATGGAATGGAAATTAACTCAGTCTGTGGCAAATGGTGCACAA
ACTAACACAGAGGAAGTTATTATGTGTGACTCGCTTCAAGATCCACAGAACCA
AGACAGGTTTATCACTAATGTAACAGCTGTATAGAAAATGTGAATGCAAACTGCCATT
TAGATAATGTCGTATACTGTCAGAAATTAATAAAACCTTAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTGTACAAGAAGCTATAAGAAATTCTGTGACAGATCTTCAACAAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCACTACTAGGTTACAAGAACACA
CTATCTAGCCAAGGACACCTTCTAACTCAACTTACTGAATTGTAACCGTGAAT
AATTGTCAGGAGGATACATTGTGAGTTGGGACAAGTTCTGTGAATCATGGAGAAC
ACATCTTCAACAAACTCATGCAACACTGTTGAAAGCTACTTTAAGGATATCCCAGAGCTCC
AAAAGACCACAGAGTTGTACAAATTCAACCGGATATACTGCTTCAAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCTCATCTCATGAAATGGATGGAGACTACATAAATATT
TCCAAGAGAAAAGCTGCAATGATTCAATGGCAATGTCAGTTGCAATTGAT
AGAGTATTGTCCTTGTCTTCACTCTGACAATTCTTATTGAAACCTCAAATATTGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCAATGAGCTAAACCC
GGCTACATTATGAACTTGTGAAACATTACATTAACTGATCGAAAGGTCAACAGATA
GGTATAGGAGTCTATGTCATTGAAATTACTCACCTGATACCATGAAATGGCAGCTGGCT
TCAGAGGGCTGTGAGCTGACATCTCAAAATGAGACCCACACTCATGCCGTGAACTCACCT
GACACATTGCAATTGATGTCCTCTGGCTCTTCATTGGTATTAAAGATTATAATT
TTACAAGGATCACTCAACTAGGAATAATTATTCTGACTGATTGCTTGCCATATGCACTT
ACCTTCTGTTCTTCACTGAAATTCAACGACCCAGGAAACAACTTCAACAAAATCTTGTG
TAGCCTATTCTTGTGAACTTGTGTTCTTGTGGGATCAATACAAATACTAAAGCTCT
TCTGTTCAATCATTGCAAGGAGCCTGACACTACTCTTTAGCTGCTTTGCATGGATGTC
ATTGAAGGCAATCATCTCATCTCATGTTGTGTCATACACAAAGGGATTGGCA
CAAGAATTATATATCTTGGTATCTAAGCCCAGCGTGGTAGTTGGATTTCGGCAGCAC
TAGGAGTACAGATAATTGGCAACCAAAGTATGGCTTAGCACCCAAAACAATT
TGGAGTATTAGGAGCACATGCTTAATTCTCTGGATCTCTTGGCTTTGGAGTCAT
CATATAACAAAGTTTCTGTCACACTGCAAGGGTTGAAACCAAAGTAGTTGCTTGGAGAACA
TAAGGGTCTTGTGCAAGAGGAGCCTGCTCTCTGTCTCTCTCGCACCACCTGGATCTT
GGGGTCTCCATGTTGTGCAACGATCAGTGGTACAGCTTACAGTCTTCAACAGTCAGCAATGC
TTTCCAGGGATGTTCACTTCTCTGTGTTTATCTAGAAAAGATTCAAGAACAA
ATTACAGATTGTCAAAATGTCCTCTGGTTGGATGTTAAAGTAAACATAGAACATG
GTGGATAATTCAACACTGCAACAAATAAAATTCCAAGCTGTGATGACCAATGATAAAAAA
TGACTCATCAAATTCTCAATTAACTACTAGACAAAAAGTATTAAATCAGTTTCT
GTTTATGCTATGAAACTGTGATAATAAGGTTAAATTATGATCATATAGATATACTATGT
TTTCTATGTAATGTTCTGTCAAAATAGTATTGAGATATTGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCAACCAAGGAAAGTCTTCTAACACAGAGAACATATGAA
TGTCTGAGGAAACACTGGCTTGTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACTCGGTAAATGAGCTCATTACAGAAAGTGGAACATAAGAGAACATGAGGAGA
ATATCAAACAGTGAAGGAAAGGAAATGATAAGATGTTGAATGAACTGTTTCTGTGAC
TAGCTGAGGAAATTGTCACATAAAACACTTAGACTCTGTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLVVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGYYCMCVPGRSSNQDRFITNDGTVCIENVANCHLDNVCIAA
NINKTLTKRISIKEPVALLQEVEYRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL
SNSTLTFVKTVNQFVQRDTVVWDKLSVNHRRTLTKLMHTVEQATLRLISQSFQKTEFDT
NSTDIALKVFFFDSYNMKHIIHPHNMMDGYINIIFPKRKAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPKQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELTISNETHTSCRCHNLTHFAILMSSGPGSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSIIAGL
LHYFFLAFAWMCIEGIHLYLIVVGVVIYNKGFLHKNFYIFGYLSPAVVVGFSALGYRYYG
TKVCWLSTENNFIFIWSFIGPACLIILVLVNLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTIWFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATAATGGATGGAGACTACATAAATATTTCCAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTAAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAGAGTCATATCTCAGTAATTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAAGGAAACCTGGGGCGTGCCTGGGGAGGAGTCCCCAACCGGGCG
CTAAGCGAGGCCCTCCTCCCGAGATCCGAACGCCCTGGGGGGTCACCCGGCTGGGA
CAAGAAGCCGCCCTGCCTGCCCCGGGGGGGGGGCTGGGGCTGGGGCGAGGGGG
GGTGTGAGTGGGTGTGCGGGGGGGGGAGGGCTTGATGCAATCCCGATAAGAAAATGCTCGGG
TGTCTTGGGCACTTACCGTGGGGCGTAAAGGGCTACTATATAAGGCTGCCGGGGGG
CCGCCGCCTCAGAGCAGGAGCGCTCGTCCAGGATCTAGGGCACGACCATCCAACCC
GGCACTCACAGCCCCGCAAGGCATCCCGTCGCCCGCAGCTCCCGCACCCCCATCGCGG
AGCTCGCCCGAGAGCCCCAGGGAGGTGCCATGCGGAGGGTGTGGTGGTCCACGTATGG
ATCCCTGGCCGCCTCTGGCTGGCCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGG
CCACGTGCACTACGGCTGGGGCACCCATCCGCCTGCCGCACCTGTACACCTCCGGGGGG
ACGGGCTCTCCAGCTGCTCTCGCGCACGGGCTCGTGGGACTCGCGCGGGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGGGACCCGTTGGGCATCAAGGG
CGTGCACAGCGTGGGTACTCTGCATGGGCGCGACGGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGGAGATCGCCCAGATGGCTAACATGTGTACCGA
TCCAGAGAACGACCCTCCGGTCTCCCTGAGCAGTGGCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTCCACTCTCATTTCTGCCTCATGTCGCCATGGTCCCAGAGGAGCTG
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTGCAAGGGACTGGAGGGCTGGAGGACTCCAGTTTGAGAA**TACT**
GAGACCATGGGGGCTTCTACTGCTGCCAGGGCTGTGGTACCTGCGAGCGTGGGGAGC
TGCTTCTACAAGAACAGTCTGAGTCACGTTCTAGTTAGGAGAAAACATCTAGAA
GTTGTCATATTCAAGGTTTCCATTGGCAGTCCAGTTCTAGCAATAGACTTGTCTGAT
CATAACATTGTAAGCTGTAGCTGCCAGCTGCTGCCAGGGCCATTCTGCTCCCTCGA
GTTGCTGGACAAGGCTGCACTGTCTCATGTTCTGTTGAATACCTCCATCGATGGGAAC
TCACCTCCATTGGAAAAATTCTTATGTCAGCTGAAATTCTCTAATTTCATCATCATT
CCCAGGAGCAGCCAGAAGACAGGAGTAGTTTAAATTCAAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCTACTCAACCCCATGTGGAAATTGATCTATATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCAGGCCAGAACGACTGACTGGAGCAGGCATGCCACCG
CTTCAGGAGTAGGGGAAGCTGGAGCCCCACTCCAGGCCCTGGGACAACCTTGAGAAATTCCCC
CTGAGGGCAGTTCTGTCATGGATGCTGCTCTGAGAATAACTTGCTGTCCGGTGTACCTG
TTCCATCTCCAGGCCAACGCCCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCAACCTTATGTCACCTGCACTTCTTGTCAAAAATCAGGAAAGAAAAGAT
TTGAAGACCCCAAGTCTTCAATAACTTGCTGTGGAGAGCAGGGGGAGACCTAGAAC
CTTTCAGGCAACTGGTTTCAACATGATATTGAGTAATTATTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAATTATTTGATATGTAACTGAGGTTG
TTTGATATTAAAGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSDMPFGLVTGLEAVRSPSFKEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCAGAAGTTCAAGGGCCCCGGCTCTGCGCTCCTGCCGCCGGACCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCAGGAGGAGCCGCCACGCCCTCCTGCTG
CTGCTGCGCTACCTGGTGGCTGCCCTGGCTATCATAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTAGCCTGCAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGAAGAAACTGGGTGGAGGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCAGTCAGTGGAAAGTATTAGTGGCTCAGCAGTT
CCATCATGTGAAGTACCCCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAATCCAGCTCTGAATAACACATGGTTAACGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAACTGGAACT
CTGCAATTAAACTGTTCAAAGTGGACACTGGAGAAATTCTGTGAAGCCCGAATTCT
TGTTGGATATCGCAGGTGCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTGTGGCCTGGTGTATGCTAT
GCTCAGAGGAAGGCTACTTTCAAAAGAAACCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAAATGCGAGTGGCTCACGCCCTGAATCCAGCAGTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAACAAAAATTAGCTGGCATGGTGGCATGTGCCCTGCAGTTCAAGCTGC
TTGGGAGACAGGAGAAATCACTGAAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCAGCCTGGTAACAGAGCAAGATCCATCTCAAAATAAAAATAAAATA
AATAAAATCTGGTTTACCTGAGATTCTTACAATAATAGCTTGATATTCT

FIGURE 24

MARRSRHRLLLLLRLYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTG EYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA AAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACAGCCCGGACCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTTCATCTAAATAA
ATGAAATTACTCAATCCTCATGACCATCTACATACATCCACCTCAGAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACTCTCTTCTCCAAATATGCATGACATTGGCAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAACCTTGTGGTTCTATGGCATTCA
TTTGACAAATGCAAGCATTCTCTTATCACTCAGTCTCTTGAACTTACTAGCACTGACTG
TGGAAATCCCTTAAGGGGCCATTACATTTCTGAAAGAAGAAGCTAAGATGAAGGACATGCCACT
CCGAAATTCATGTGCTACTTGGCTTAGCTACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCAACGGTTATGTACGTGTGAAATCAGGCCCTGGTTACACCCAGATCCATTAT
ATGGAAGGCACTACAGTGGATTGTAATGATTAGGTTCTTTAACTTCCCAGGCCAGATTGCC
AGCTAAACACACAGATTCTCTCTCAAGACTAAACATATGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCTGGATTATCTCAAAACAAATTATCTTCACTGCAACCAAT
ATTAATGAAAAAAAGATGCCCTCAGCTCTTCTGTGTAACCTAGAGGAAACAAACTTACTGA
ACTGCCGTGAAACTGCTGCCAAGTAGCAGACAACTTACAAGAAACTCTATATTAACTACAAC
TGCCTTCTCACAAATTCTCACCTGGAGCTTATGGGCTCACTATAATTCTTCACTTC
AATTCAAAATGATTGAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT
TCTGATGATTGGGAAATCTCAGAATCAAAGACATGAACCTTAAAGCCTTCTTCA
ATCTTCGCAAGCTGGTTATAGCTGGTATAACCTCAGAAATACCAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAAGCATCTCTTTACGATAACAGGCTTAAAGTACCCATGT
TGCTCTTCAAAAGTGTAAATCTCAAATTGGATCTAAATAAAATCTTAAATAGAA
TACGAAGGGGTGATTCTGAAATGTCACACTTAAAGAGTGGGATAAATAATATGCC
GAGCTGATTTCATCGATAGTCTTGTGTTACATTCACTTCAAGCTGGAGATTAAAGAAC
TACTAACAAACCTAGATTGTCTTACATTCACTTCAAGCTGGAGATTAAAGAAC
AATCACTCATGTCGAACGCAACTGCTTCAGTGGCTCTGTAACCATGGTACCTGTCTG
CCAAACCTCAAGGAAATCAGCATCACAGTAACCCATCAGGTGTGACTGTGTCATCG
GATGAACATGAACAAAACCAACATTGATTCACTGGAGGCCAGATTCACTGTTTGCG
CACCTCGAAATTCCAAGCTTGGCAAGATGTCAGTGCATTTCAGGGACATGATGAAAATTGT
CTCCCTCTTATAGCTCTGAGAGCTTCTCTTCAATCTAAATGTAAGAGCTGGGAGCTATGT
TTCCTTCACTGTAGAGACTCTGCAAGAACACAGCTGAAATCTACTGGATAACACCTCTG
GTCAAAACCTTGGCTTAACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAATGGCGTAACTCCAAAGAAGGGGTTTATATACCTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTGTGTTATGATCAAAGTGGATGATCTTCCACAAGATAACATG
GCTCTTGAATATTTAAATAAGAGATATTCAAGGCCAATTCACTGGGTTGTCCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGAAAGTGTCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTTATGATATTCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAATGTCAACCCAAAGGTTGCACTGTGATCAAAGAGTATGAAAAGAATAATAC
CACAAACATTATGGCTGCTTGGAGGCCCTCTGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCCTCTCCAGAAATGAACTGTGATGGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTATAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAGTAAAAGCAACTGTGTTAGGTTACCAACAAATATGTCT
AAAAACACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITLVLQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQQTNTIAKIEYSTDFPVNLTCGLDLSSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPPLINLRSVLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSIAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYGHTIESLPNLKEISIHSNPIRC
DCVIRWMNNMKTNIRFMEPDSDLFCVDPPEFQGQNVRFDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMITKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKAASKILKSSVKWTAFV
KTEENSHAAQSARIAPSVDVKVYNLTHLNPSSTEYKICIDIPTIYQKNRKCVNVTTKGLHPDQE
YEKNNTTTLMACLGGLGIIGVICLISCLSPEMCDDGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSCLKVAKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAAATAATGAAGAGACATGTGTTAG
CTGCAGCCTTTGAAACACCGCAAGAAGGAATCAATAGTGTGGACAGGGCTGAACTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTATGCTGACATTCCAGC**ATGAATCT**
GGTAGACCTGTGGTTAACCGTCCCTCCATGTGTCCTCTCAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCACAAGGGCTGCTTGTCTCCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAACTCAAGGAAATACCTAGAGATCTCCCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTGCGAAGACTCTGGACTGTGTCGACAATCGGATTCAAAG
TGTGCAACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCAATCATGAGACAGCCAC
AACGTGATCTGAAAACGTCCTGTTGGATGAACTGTCGGCAGACCATTCCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACCTGAATCCCTGCCAAGCAGGAGAAGAAAGCAGATGA
ACCTGATGATATTGCACTGTGGTAT**AGTGTCCAAACTGACTGT**CATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCCTCCATCCATTGTAACATTTGAA
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAAACAAACACTACAACA
TAAAATTTGAGTTAGGTATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTATTTTT
AATTAAAAGCAAATAAGCTTAACCTGAACCATGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFSVLMILCFHSASMCPKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDNSQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLSDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHNETAHNVICKTSVLDEHAGRPF
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

FIGURE 30

MQVSKRMLAGGVRSMPSPILLACWQPILLVLGSVLSGSATGCPPRCESAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRNSRLKLIPLGVFTGLSNTLKQDISENKIVILLDMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYPLDTMTPNCLYGLNLNTSLITHCNLTAVPYLAVRHLYLRFLNLSYNPISTIEGSMILHEL
LRLOQEIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTLEESVFHSVGNLETLLIDSNPLA
CDCRLLWVFRRRWRRLNFNRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKM

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACACGCGTCCGCACCTCGCCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC
ATCGTAGTCACCCCTCCCCATCCCAGCCCCGGGGATTCAAGCTCGCCAGGCCAGCC
AGGGAGCCGGCGGAAGCGC~~G~~**A**TGGGGGCCCCAGCCCTCGCTCCTGCTCCTGCTCCCTGC
TGTTCGCCCTGCTGCTGGGGCCCGGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGCTCAAGTGCCAAGTGAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCCCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTACAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCAGTACACCTGCTCAATCTTCACTATGCCGT
GCGAACATGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCACATCATCTGGTT
ATAAAATCTTCAATTACGGGAAAAGACACAGCCACCCCTAAACTGTCACTTCTGGGAGCAAG
CCTGCAGCCCCGCTCACCTGGAGAAAAGGGTACCCAAGAACCTCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAACGAGCTGGTACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCAATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCTCGTGAAGGGCCAGAAGCTGGCTACACTGTGAGGGTCCGGCAATCCAGTC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCCAACAAGAGTGAACAGTGGCACCTACGGCTGCACAGGCCAC
CAACATGGGAGCTACAAGGCTACTACACCCCTAATGTTAATGACCCAGTCCGGTCC
CCTCCTCCAGCACCTACCGCATCAGGGGATCGTGGCTTCAATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCACTACTTGATCCGGACAAAGAACCTACCTGACACA
TGAGGCAAAGGCTCGACGATGCTCCAGCAGCGGACAGGCCATCATCAATGCAAGGGCG
GGCAGTCAGGAGGGAGCACAAGAAGGATATTCTAC**T**AGAGGCGCTGCCACTTCTGC
GCCCTCCAGGGCCCTGTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCCGCTGCTCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTGGGTGCGTTTTGTACTCGGTTGGAAATGGGAGGGAGGGAGGGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCAATTGGTTATTATTGTAAACATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAACAA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVLADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAACCCCTTTCCTCTCCTTCTGG
CTTCGGACATTGGACCAACTAAATGAACCTGAATTGTGTCCTGTCGAGCAGGATGTCGCTG
TTACTTTGIGATGAGATCGGGGATGAATTGTCGCTTAAAGGGTCTGTTGGATTCTGTT
GCTGGAGACGCTCTTCTGGCGCTGGAAACGTTACAGGGGACCTTGCAAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAGGCCCTCAC
AGTCTGCAGCGTTTCACTGCCCGACTTCCCAGTTAACCTTATTCCTGCATGCCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACTTTATAATGCGGTTAGTTGACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTCTGGCTGCAAGCTGGTAAAAGG
CTGCACACATCAACAACAAGAATCAAGTCTTTCGAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCAGGCTGATTTAATTACAGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATGCCAACCTACCTGCCAAC
GTGTTCCAATATGTCGCCATCACCCACCTGCACCTCCGGTAACAGGCTGAAAACGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTCTAGAGGATAACCC
GGGACTGACCTGTGATCTGCTCTCCCTGAAAGAATGCGTGGAAAACATTCCAAGAATGCC
CTGATCGGGCGAGTGGTCTGCAGACGGGCCCCCAGACTGCAGGGTAAAGACCTAACGAAAC
CACCGAAGCAGGACTTGTCTTGGAAAACCGAGTGGATTCTAGTCTCCCGGCCCTG
CCAAGAAGAGACCTTGCCTGGACCCCTGCCAACTCTTCAAGACAAATGGCAAGAG
GATCTGCCAACACAGGGTCTGCTCCAAACGGGAGTCAACAGATCCACGGCAACTGGCAGAT
AAAATCACAGGCCCCACAGCAGCGATAGCAGGGTAGCTCAGGAAACAAACCCCTAGTAAAC
GTTTACCTGCCCTGGGGCTGAGCTGCCGACACATCCCAGGGTGGGTTAAAGATGAAC
TGCAAAACAGGAACGTTGAGCAGCTTGGTATTGAGGCCAAGCTCTTAACGTGCAAGGA
GCTTTTCTAAGAGATAACAGATCCACAGCATCCGACTTGTGGATTACAAGA
ACCTCATCTGTGGATCTGGCAACATAACATCTGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
AAACATTCCGAGCTTCAATGGCATGCCAACACTGGAGCTGGAGTACAACGCTCTCAGCTCA
TCTCCGGGCACTTCAATGGCATGCCAACACTGGAGCTGGAGTACAACACCTG
CTGAGGGTCTGCTGTGGAGCTGTCGCTGGGCTCCTCTCTAAACTCAGCCTGCACAA
CAATTACTCTATGACTCTCCGGTGGCAGGGGCTGACAGTTAACCTCCATCATCCAGA
TAGACCTCCAGGAAACCCCTGGGAGTCTCTGGCACAATTGTCCTTCAAGCTGGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGGCCACTCAAGTGTGAGACGCCGGTAACTCTT
TAGAAAGGATTTCATGTCCTCTCCAAATGAGACTTGTGAGCTGGAGTACAACGCTCT
CGCCCGAGTAACTTCGCAACAGTAAAACAGCACTGGGTTGGCGGAGACCGGGACACTCC
AACTCCACTTGAACACAGCAGGGTCTGCTGGTCTGGGACTCTGCTGTGGT
GTTTGTACCTCCGCTTCAACGGTGGGATGCTCGTTATCTGAGGAACGGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCCTCCGGTCCGAGATTAACTCCCTACAGACAGTCTG
GACTCTTCACTGGCACATGGGCTTACAACGAGATGGGTTGGCGGAGACGGGACTCT
TGGCTCTCACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGG
ATACATCTTCCCAACGGCAGGCCACCCGGGGCTGGAGGGGCGTGTACCCAAATCCCGCG
CCATCAGCCCTGGATGGGCAATAAGATAATAACTGTGAGCTGCCACAACCGAAAGGGCT
GACCCCTTACTAGCTCCCTCTGGAAACAAAGAGCAGACATGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTCTTGTGAGAGGCCCTTGTGAGAAAGGCCAGCACGACCCCTGCTGGAG
AACTGAGCTGGCCCTCGCCCTCGGCCCCGGGCTGTGGGGTGGATGCCGGTTCTATAC
ATATATACATATATCCACATCTATAGAGAGATAGATATCTATTTCTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTGGCTACGCAGGGATGGGAGTTGCACAAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSCLCFAAGNVITGDVCCKEIKCSCNEIEGDLHVDCCEKKGFTSLQRFTAFTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGNLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIRDPGAQFDLNKLEVLLINDNLISTLPANVFQYVPITHDDL RG
NRLKTLPYEEVLEQIPGIAEILLEDPNWDCDLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLAPPAAQEETFAPGPPLPTPKTNGQEDHATPGSAPNGGT K
IPGNWQIKIRPTAAIATGS SRNKPLANS L PCPGGCSDH TPGS GLKMNCNNRN VSSLA DLKP
KLSNVQELFLRD N KIHS I RKS HFVD YK N L I LLD LGNN NIA TVE NN TFK N L L DLR WLYMDS NY
LDTLSREKFAGLQNLEYLNVEYN A I Q L I L P G T F N A M P K L R I L I L N N N L L R S L P V D V F A G V S L
SKLSLHN NY FM YL P V A G V L D Q L T S I I Q I D L H G N P W E C S C T I V P F K Q W A E R L G S E V I L M S D L K C
ETPVNFFRKDFM LLSN D E I C P Q L Y A R I S P T L T S H S K N S T G L A E T G T H S N S Y L D T S R V S I S V L
VPGLLL V F V T S A F T V V G M L V F I L R N R K R S K R R D A N S S A S E I N S L Q T V C D S S Y W H N G P Y N A D G
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTCGTCCCCGTACCCGGCGCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCTGGCAGCGTCCGCACACATTCTGTCCGGCTAAGGAAACTGTTGGC
CGCTGGGCCGGGGGGATTCCTTGGCAGTTGGGGGCTCGTGGAGCGAGGGGGGGGG
AAGGGAGGG
AGCTCTGGCTCCTCGAGGGGGAGATCAACAGTTGGGGAGCAGCTCGCTGCGGGGGCTCAG
AGAATGAGGCCGGCTTCGCCCTGTGCCCTCTGGCAGCGCTCGGCCGGGGGGGG
CGGCAGAACACCCCACTGCCGACCGTGTGGCTCTGCCCTCGGGGCTGCTAAGGCCCTGC
ACCACGCTACCATGAAGCGGCCAGGGCCGAGGAGGCCATCTGCGAGGTGGGGCGCTC
AGCACCGTGTGGCGGCCAGGCTGCCCTGTGCTCGCTCGGGGGAGGGCCCAGG
GCCCGGAGGGGCTCAAAGACCTGTGTTCTGGGTGCGACTGGAGCGCAGGCCTCCACT
GCACCCCTGGAGAACAGGGCTTGGGGGTTCTCTGGCTGTCCCTGGACCCCGGGCTC
GAAAGCGACACCGCTGAGTGGGTGGAGGCCAACCGTCTGACCGCGCGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTGCAAGGCCAGGCTGGAAAGGAGATGCGATGCCACCTGC
GCCGCAACGGCTACCTGTGCAAGTACCAAGTTGGAGTCTTGTGTCCTGCGCCGCCCGG
GCCGCCCTAACTTGAGCTATCGCGCCCTTCCAGCTGCAACAGCGCCGCTCTGGACTTCA
TCCACCTGGGAGGGAGGTGAGTGGCTCTGCCGGGAGCAGCTCCGATCTCAAGTACTTCA
TCGGAGAACATCGCGCTCGCTGGGACAAACTCTCGGGCGATGTTGTTGTCCTGCC
GGGAGGTACCTCCGTCTGGCAATGCGAGCGAGCTCCCTAAACTGCTTAGACGACTGGGAG
CTTGCCCTGCAATGCTACGGGCTTCCAGCTGGGGAGGACGCCGCTTGTGACCA
GTGGGGAGGACAGCGGACCCCTGGGGGACGGGGTGCACCCACAGCGCCGCCG
GCAACAGCGCCGAGAGAACATGGCCAATCGGGCTGACAGGAAGCTGGAGAGAC
ACCACTTGCTCCCTGACAAGAACATTCACTGATCTTCTGAGATTCCCTGATGGGAT
CACAGACGACGATGTCACCCCTTAAATGCTCCCTTAAGCCGAGCTAACGGCACTATCACC
CCATCAAGGGAGCGTGATTCCAAGTTAACTCTAGCAGCTTCTCTGCCACTCCTCAGGCTT
CGACTCTCCCTCTGGCTGTCATATTGTGAGCACAGCAGTAGTGTGGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTGCTTTCAGGAAAGCCCTTCCAGCCA
AGGAAGGAGTCTATGGGCCGCGGGGCTGGAGAGTGTACCTGAGCCGCTGTTGGGCTC
CAGTTCTGCACATTGACAAAATGGGGTGAAGTCCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGTGGCGGAGTCCCTCTGGCTCTAGTGTGCA~~TAGGAAACAGGGG~~
CATGGGCACTCCCTGCAACAGTTTCTACTTTGATGAAACAGGGGACCAAGAGGAATTAC
TTGTGTAACTGACAATTCTGAGAAATCCCTCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
GAGCTAAATCAGAACACTGCACACTCCCTCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTGATACTGGGGGACGGGGTAGTGTGGGGAGAGATAATTCTTATGTTTATTGGAGAA
TTGGGAGAAGTGATTGAACTTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGCAATCCAGGGAAAAAAATAAAAATAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLFLWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPORSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPGA
ASNLSYRAPFQLHSALDFSSPPGTEVSALCRGQLPISVTCIADEGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEGQFTLGGTGVPTRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATQAFDSSSAVVFIFVSTAVVVLVLTMTVVLGVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKGDCDLRDRAGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTCA GAGCTGGCCTGTGGCTGCCAGAGCAGCTCC CAGGGAAACTAAG
CGTCGAGTCAGACGGCACCAT AATCGCCTTAAAGTGCCCTCGCCCTGCCGGCGGTATC
CCCCGGCTACCTGGGCCCGCCGCGCGTGC CGCCGTGAGAGGGAGCCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCCGGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGCTGTGCGCCGGCGCCGGCGTGGGTGCAAACCCGAGCTCTACGCTGCCATGA
GGGGCGCGAACGCGCTGGGCCACTCTGCCCTGTGCTGCCGCA CCCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTGTTTCAATGTGTGAGTGCATTCCTA TCTGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATGCAAAATGTACTTGGAAAATCA
CAGTCCCCAGGGAAAAGTAGTGTGTTCTCAAATTCGAGTCA TAGACCTCGAGAGTGA CAAC
CTGTGCCGCTATGACTTTGTGGATGTACAATGCCCATGCCAATGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCCGGCTGGAGCCCTGTGCTGCCAGTGGCAACAAAGATGATGGTGCAGA
TGATTCTGTGCAACACAGCTGGCAATGGCTTCACTGGCCATGTTCTCGCTGTAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTCCGGCTCTTTAAAAC
CCCCAACTGGCCAGACGGGATTACCTCTGCAAGGAGTCACTTGTGTGCGCACATTGTAGGCC
CAAAGAACATGCTTATAAGATTAAGTTGAGAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGCTGTGTTAATGCCGGGAAGTCAACGATCTAGAAGAATTGGAAA
GTATTGTGTGATAGTCCACCTGCCAATTGTGTCAGAGAAATGA ACTTCTTATTCA GT
TTTATCAGACTTAAGTTAATCAGATGGTTTATTGTGCACTACATATTCA GGCCAAA
AAACTGCTTACA ACTACAGAACAGCGCTGTCA CACCACATCCCTGT AACCACGGGTTAAA
ACCCACCGTGGCTTGTGCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGA CTTTGTATTAGCGGCACTGT TATCACAACCATCACTCGCGATGGAGTTG
CACGCCACAGTCTCGATCATCACACATCTACAAAGAGGGAATT TGGCGATT CAGCAGGCCGG
CAAGAACATGAGTGC CAGGGTCACTGTGCTGCAAGCAGTGCCTCTCCCTCAGAACAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGAACAGAACATCAGAACGCTCTGGATGCCCTTAAAAAATAAAGCAATG
TAAACAGTGAACTGTGTCATTAAAGTGTATTCTGCATTGCTTGAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTAAAAATACATATTCTGAAAGAGGATTGCCAAGATGG
GACTGCTTGA CTTCACATGATGGAGGTATGAGGCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCCTGCTGCAAGGGAGCAGCTATCTGATTGGAAACCTGCCGACTT AGTGC CGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTTATTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTAAGATGTCAAAAAAAGATTTAGAAGTGA CAATTATTTAGT
GTTATTGTTTACCTTCAAGCCTTGCCCTGAGGTGTACAATCTGTCTTGC GTTTCTA
ATAATGCTTAATAAAATTTTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTEQPVTTFPVTTGLKPTVALCQQKCRRGTLEGN
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGAGCGCTGGCGGCCACGGCGCCCGGGCTGGCGGTGCTTCTT
CCTTCTCGTGGCTACGAGGGCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTCTCTGGGCTCAGCCTCTCCTCAACCTCCAGGACCTATCTG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCAGCCCATCCGTGTACACCTG
CCGGGGACTGTTGACAGCTTAACAAGGGCTGGAGAGAACATCCGGACAACTTGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATAAAAGACAGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTCGAGTGCCACCGCCTGTTGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTGTGCTGCCCGCAGGCACCTTCGGGCTCTGC
CTTCCCTGTCTGGGGAAAGAGAGGCCGTGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGCACTGTGACTGCCAACGCCCTACGGGGTGAGGCCGTGGCC
AGTGTGGCTTGGCTACTTGAGGCAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCACTCACCTCAAGTGTGAGACATTGATGAGTGTCAGGCCACAGAGGGAGCCA
ACTGTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCA
GCCTGCCCTAGGCTGCATGGGGCAGGGCAGGTCGCTGTAAGAAGTGAGCCCTGGCTATCA
GCAGGGGGCTCCAAGTGTCTCGATGTGGATGAGTGAGACAGAGGTGTGTCCGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTACGCTGCATCTGCGCAGGGCTACAAGCAG
ATGGAAGGCATCTGTTGAGGAGCAGATCCCAAGAGTCAGCAGGCTTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGTGCTGCAGCAGATGTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTGGTGTACCGCCATCTCATGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCGAGTGACCGTGTGGAGGGCTCATCAAGGGCAGA
ATCGCGGCCACCACCTGTAGGACCTCCCTCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCCTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGACTGGCAGGCTTACAATGTGTA
ATTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCTGCACTGCCAGTTCCCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGVLPAVLWGSLFLNLPGPWIWLQPSPPPQSPPPPQPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEENLSKYKDSETRLVELEGVCSDKSFECRHLLELSEELVESWWFHKQQEAPDLFQWLCSDLKLCCPAGTFGPSCLPCPGGERPCGGYQGCEGEGRGGSGHCDQCAGYGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKVDIDECTEGANCAGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFGIIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179, 177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289, 326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCTCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGACTCTGGTGTTCGCCCTGGCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCGGAGCTGAGCTCAAAGAGGT
GCCACCCCTGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCGTGAAGGCCAGT
ACGTGGCCCTGCTGCAGCCCAGCCACGGGACCGCTCCGCGAAAGAGGTTCAAGGCCAGGC
TTCCGAGAGGTGGCCGGCAGGTTCCGGCGTTGGAGGGCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCTGGCGTGCAGGCCCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGCTGTCCCCCGCAGGCCCGGGCC
CGGGTGACCGCTGAGTGGCTGCGCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCACGAGAGCGGCTGGAAGGCCCTGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCGCTGCTGCTACAGGTGTCGGTGAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGTTGCCCTCGCAGGGGGC
GCCAGCCGGCTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCAGCTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGTCGCCGCCAGGAG
ATGTAATTGACCTGAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGGCCCGGGCTT
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCCGAGGCCCTGGCCTCAAGTGGC
CGTTCTGGGCCCTGACAGTGCATGCCCTGGAGACTGACTCGTGCCTGACATGCTGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGCTCGATGGTGCCTCGAAGGAGGCTCAGCCATGGCGCTAGTG
TAGCCATCGAGGGACTTGAATTGTGTGTTCTGAAGTGTGAGGGTACCGAGGAGAGCTG
GCGATGACTGAACCTGCTGATGGACAAATGCTCTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAAGTTACCTCACCTAATTTTGCTTCTCAGGAATGAGAATCTTGGCCACTGG
GAGCCCTTGTCAAGTTCTCTATTCTTATTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAAACCTGAGGGCAGAAAGCCCANTGTGTATTGTTACTTGTCTGTCA
TGGATCTGGCTAAAGTCTCCACCACCACTCTGGACCTAACGACCTGGGTTAAGTGTGGG
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPEQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTCGGCGCTGGTGTCACTGGCTGATCGC**ATGGGGACAAA**
GGCGCAAGTCGAGAGGAAACTGTTGCTCTCATATTGGCGATCTGTGCTCCCTGG
CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTGTCTCTGTGCCACTCGGGCTTTCTTCTCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGAACCAACCAGACTCGTTGCTATAATAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTCTTGCCAACTGGTATCACCTCAAGTCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCCATCCAAGGCTACAGTTAACATCCCCCTCTGCCACCATGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT
GGGATAGTGTGCTCACGAATCCAAAAGCACCCCGTGCCTCAGCACTCTTCTATGTCT
GAATCCCAACAGGAGAGCTGGTCTTGATCCCCCTGTCAGCCTCTGATACTGGAGAACATA
GCTGTGAGGCACGGAAATGGGTATGGACACCCATGACTCAAATGCTGTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGGGAGCCGCTCTGTAACCTGATTCTCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTAGCCGAGGCCACTTGACAGAACAAAGAACAGGAA
CTTCGAGTAAGAAGGTGATTACAGCCAGCTAGGCCAGTGAGGAGATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCTGGTCCGCTCACCGCCTATCATCTGCATTGCTTACT
CAGGTGCTACCGGACTCTGCCCTGTATGCTGTAGTTACAGGATGCCATTGGTCTTC
TACACCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTCCCC
ATCCCTCTTCATGCCCTCCCTTCTTCTTACACTGCTGAGTGGCTGGAACATTGTTAAA
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAACCTGGGATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATTTGAATAGGTATCTTGAGCTTGGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTCTGAATACAAGTCAGTGAATTGACTGTCTG
GGAAAATGGGAGCTTGTGAGGAGACATAGTAATTTCAGAGAACCTGAAGC^{AAAAG}
GATTAAAACCGTGCTAAAGAAAAGAAAAGACTGGAGGCTGGGCGAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTGGGATCAGCCTGACCA
ACATGGAGAACCTACTGGAAATACAAAGTTAGCCAGGCACTGGTGGTGCATGCC
CCAGCTGCTCAGGAGCCTGGCAACAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGEELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGA CAGC **ATGAGCGCGGTTGGATGGCGCAGGTTGGA**
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCCCTTCACCCGACCTCTGCCAGGCCGAGGCCCGAGCTCAG
GCTCGCCACCCACCAAGTTCCAGTGGCGCACCAAGTGGCTATGCGTGCCTCACCTGG
CGCTCGACAGGGACTTGAGTCAGCGATGGCAGCGATGAGGAGGTGAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCTCCCTGCCCTGCAACGGCGTCA
GTGACTGCTGGGGAACTGACAAGAACTGCGCAACTGCGAGGCCCTGGCCTGCCCTAGCA
GGCAGGCTCCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTTAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGCGGAATGCCACATCTC
CTCTGCCGGAGACCAGTCTGGAAAGCCCACTGCTATGGGTTATTGCGAGCTGCTCGGTGC
TCAGTGCAGCCTGGTCAACGCCACCCCTCTCTTGTCTGGCTCGAGGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAC
CTCGCTGCCCT**TGAGGACAAGCACTTGCCACCCGTCACTCAGCCCTGGCGTAGCCGGACA**
GGAGGAGAGCAGTGTGATGCCGATGGGTACCCGGGACACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAAGAATGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC
GGGCTGGCCCAGGCAGCTCCAGGGGTAGAACGCCCTGCTTAAGAACACTCCCTGCTG
CCCCGTCCTGAGGGTGGCATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAAASPLSTPTSAQAAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDGSDEEECRIEPCCTQKGQCPGGLPCCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSPL

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCGGTCTCGCTCGCTCGCGCAGCGCGGAGCAGAGGTGCGCACAGATCGGG
GTTAGACTGGCGGGGGAGGAGGCGAGGAGGGAAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCAGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCACGAGAACCTCAGTCCCCAGAGACTCTTG
GCCGTGATCTGTGGTTCAAGCTGGCGCTGTGCTTCGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCCCGATTCGGAGAATGGCTCAGGACCCCAGCG
GAGGGGTTTCTTGAGGGCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTGTGATGAGGATTCAAGATCCG
TACCCGACCTACACAATATGGTTCATATTGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCAGACCTCTAGCCTCTAATGGCTATGTAACATCTGTGAGC
TCCAGACCTCTTCCGGTGGGACTGTGATCTCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTCGTGTCTGGAGTGTCTAACAAACCTTATCTGGTGTGTCAGCCCACCCGGTG
CTTGCTCTGGAAGCCCAAAGTGTCCACTACCTCCAATGGTGAAGTCACGGAGATTCTGTCT
GCCACCCGGCCCTGTGAGCGTACAACACGGAACTGTGGTGGAGTTTACTGCCATCT
GGCTACAGCCTACCAGCAGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTACGGCAACCAAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTCCAGACCAAGTTCAGGCCACTTTCCCCCAGGGGCTCCCGGAG
TTCCAGCAGTGTGACCCCTGACTTGTGGTGGTAGACGGCGTCCCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGGGTTGAGTGCCTTAGCCCCGGTACATGGCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTAGGGACACGGAA
CACAGGCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGACAAACCTGACATA
ATTGCCAGCACGGCAGAGGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCTTAAGAAACTGTGGATTAAAAAATTCCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGGTGATTCTTCTTCTTGTGGTTTAGACAAATGTAACAA
AGCTCTGATCTTAAATTGCTATGCTGATAGAGTGGTGGAGGCTGGAAGCTTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAGAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKKGATKRLCLKHFNGLGWLWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEVFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLVLVLLVILARMFQTKFAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCCACGCGTCCGCTCCGCCCTCCCCCCCCTCCCGTGCCTCGGTGGCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCCTACAGG
CCGTGCTGCCGGTGTGGCTGGGGCTGCCGGCCAGGGTGCCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTGTGCCGGGGAGGGACACAGAGGCCCTGTTA
TAAAGTCATTACTTCCATGATACTTCTGAAGACTGAACCTTGAGGAAGCCAAGAACGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAAGTTCATTGAAAACCTCTGCCATCTGATGGTACTCTGGATTGGCTCAGGAGGC
GGAGAAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGACTGATGCCAGCATAT
CACAATTAGGAACTGGTATGTGGATGAGCCCTCGCCAGCGAGGTCTGCGTGT
TACCATCAGCCATCGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGATGATGA
CCGGTGCACATGAAGAACATTCTTGTCAAATATTCTGAGAAAACCAGCAGTCC
CTAGAGAAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAAGCTGCC
CTGAATCTGGCTACAT
CTTAATCCCCAGCATTCCCTCTCTCTCTGTCACCACAGTTGATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAGAACACACC
TGGCCCTCTCTCACCAGGGAAACAGCCGGACCTAGAGGTCTACATGT
CATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCTTGT
CGGGAGAAGCCACTCCGATGACATGTTGTGACTATGACAACATGGCTGT
GAACCCATCA
GAAAGTGGTTTGACTCTGGTGGAGGTGGATTGTGACCAATGACATTATG
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGT
GAAATGAAATATG
GTTATTAGGACATATAAAAACGAAACTGACAACAATGGAAAAGAAATGATAAGC
AAAATC
CTCTTATTTCTATAAGGAAAATACACAGAAGGTCTATGAAACAAGCT
TAGATCAGGTCTGT
GGATGAGCATGTTGCCAGACCTCTGTTGGACCC
CAGCTTGGCTGTATCCTTAT
CCCAGCAGTCATCCAGCTGCCACCTTATGAGAAGGTAC
CTTGCCAGGTCTGCCACATAGTA
GAGTC
CTCAATAATGTC
ACTTGTTGGTTGTATCTAAC
TTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGGAGCTGGAAA
ACACCTCTGTTCTGCTTACAG
CAGCACATATTATCATACAGACAGAAAATCC
AGAATCTTCAAAGCCACATATGGTAGC
ACAG
GTTGGCTGTGCATCGGCAATTCTCATATCTGTTTTCA
AAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRDRGGQLVSIESEDEQKLIEKFIENLLPSDGFwigLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKTFKESREAALNAYILIPSIPLLLL
VTTVVVCWVWICRKRKREQPDPSCKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSCGEATPDDMSCDYDNMAVNPNSESGFVTLVSVESGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCGGGAGGCACAGCGTCCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGAATTGGGGGCCCGCTGAGCCCCGGGCCGCAGAAAGACTTGT
GTTGCTCTGCAGCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTTCAAGCATGCGTTGTGGACCCCAGTGCGCTCTGACCTCGCTGGCTACTGCTTCGACC
AGCGGCGGGGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTGACACGGGCTCGAGTCCTCTAAGCC
GCTCCCCTGGAGGAGCAGGTAGAGTGGAAACCCCACTATTAGAGGTCCCACCCCAAAC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCAAACCATATTCTCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGGAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTGCTGGAGAGAGACTGAGGAAGAACTATGTGAAAGACATTCCCTTC
TTTCAACCAACCTCAACCCACAGGAGGTCTTATTGCTTCAACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGACTTGTATCCAACTACCAAAAGCTGCTGGAGCCTGA
GGCAGAGAACACAGAGGCCGAGGCAGACTGCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGGATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCT
GGACAACGTGGCTGCCGAGCAGGCACACAAACCTCCAAGCTGCCCCATGCTGAAGAGATTG
CACGGATGATGCAACAGAGAGCTGTGGACACATCCTTGACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGATTGACCAAAATGGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGTTGCTGAGCTCTA
TTACCAAGGAAGGAGCAGGTGCCAGAGGGTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAAATGCCATGTCAGTTTACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYVTNLAGGPKPYSYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFPNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTASIQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHNLPSCPMLKRKFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFTIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACATAATTCGCTGGGGACCTCCCTAGCCT
TAAATTTCAGCTCATCACCTTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTAGCGTCTCCATCGGAGTGGCGCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGAAACAGAAAAGGCCAGTGGGCACCGTGTGATG
ACGGGCTGGGACATTAAGGACAGTGGCTGTGGTGTGCCCCGGACTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGGGGTGTCAGGCTGGCTGACGGCCCTGGGATTGCAAGGGACGCGTGGAGTGAA
GCACCAGAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAGCATGCC
TATGGCCGAAAACCCATCGGTGAGCCAGATGTCATGTCAGGACGAGAACCCCTTCA
GGATTGCCCTCTGGGCTTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGACAAGGGCTATGGGCTCTGCTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCCTCTCCCTCCCTCAGAGACCGGA
AATGCTATGGGCTGGGGTTGGCCGCACTGGCTGGATAATGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCACAGATTGGGGTTCACTGACTGACCCACCAAGGAAGA
TGTGGCTGTCATGTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCATGACTGCACTGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACCTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAACTACATCA
CCACCTTCCATGTCCTCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTTGTTGAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCATTTGCTCTGTTCTGAAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAATTCTGAATTGGTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTACAAATAAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCGSRLEVHLKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRILW
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGTGTCCCGGACCGTGGCGGACCGTGGGCCGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTTCTGGCTGCCCTGGG
CGCTCTCGCCCTTCCGGCTGCAGTGGTGCAGGGAAAGGCCAACCTGCAGGCTGGCAAAG
TGGTGGTGATCACAGGCCACCTCAGGGCTGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTTAATTGGTACCTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGG
TGTGGACAAGAGGGTATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAACACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCCTGCGTCCGAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCACAGGCCAGGGCGAAGGCCCTGAGGTGGCCAGGATGTTCTGCTGCTGTGG
GAAGAAGAAGAAGATGTGATCCTGGCTGACTTACTGCCCTCCTGGCTGTTTATCTCGAA
CTCTGGCTCTGGCTCTTCTCAGCCTCATGGCCTCCAGGGCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTTTAGGCTTG
TTACTCTACAAGGGCAGTTGCATTGTTGAGACTTTAATGGAGATTGTCTCACAAAGTGG
AAAGACTGAAGAAACACATCTGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTAAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLGCLGVFGIFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCIRAEEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVVEAQDVLA AVGKKKDVLADILLPSLAVYLRTLAPGLFFSILMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGIRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTVVDCSNREDIYSSAKKVKAEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLDELAALQITGVKTTCLCPNFVNNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCA CGCG TCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCCGCTC
AGGGAGGAGCACCGACTCGCCCGCACCTGAGAGCATGGTTGGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCTGGCCCCGTGATGGGCTGTTCTGCCCTTACAGAAAGT
GTTTCATGCCACCTAAGGGAGACTCAGGACAGCCATTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCCGGCTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCTCACCGTAATAAGACTTACAACAGCAACCTCTCTGTTCTC
TTCCCAGCTAGATAACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGAGCTTGTGAGACATGGGCTTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACACACGCTCTCATGCTTACATTGACAACTCCA
GTGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCACTGAGTCATGAGGACGATGT
AGCACGGGATTATACAGTCACTTACAGTTCTCAGATATTCTCTGAATAATAAAAATA
ATGACTTTTATGTCACTGGGAGTCTTATGAGGGAAATATGTCAGCCATTGCAACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAGATCAACCTGAAACGGAAATTGCTATTGGAGA
TGGAATTCTGATCCCGAATCAATTATAGGGGGCTATGCAAGAATTCTGTACCAAAATTGGCT
TGGGGATGAGAACAAAAAGTACTTCCAGAACAGTCAGTGAATGCAATGAGAACACATC
AGGAAGCAGAACACTGGTTGGCCCTTGGAAATACTGGATAAAACTACTAGATGGCAGCTTAAC
AAAGTGAATCTCTTACTCCAGAATGTTACAGGATGTAATTACTATAACTTTTGGGGT
GCACGGAACCTGGAGATCAGCTTACTATGTAATTGGAAATTCTTGTCACTCCAGGGTGGAGACAA
GCCATCCACTGGGGAACTGACACTTTATGATGGAACTATAGTTGAAAAGTACTTGCAGAGA
AGATACAGTACAGTCAGTTAACGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTAACATGGCCAACCTGGACATCATGTTGGCAGCTGCCCTGACAGAGCGCTCTTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGCAGAAAAAAAAAGTGGAAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACITCCATCAGGTAATTATTG
GAGGTGGAGGACATATTTACCCATGACCAGCCTGAGAGCTTGTGACATGATTAATCGA
TTCATTTATGAAAAGGATGGGATCCTTATGTTGGATAAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCTATTGCTGAAAAGAAAATGTAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTCTATCTGCAAGATTTTCTCATCAATAAAAATTATCTTGAACAAAGTGGC
TTTTGTTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGAACAGATGTTAAATGA
AATTGGTGGCTTGAATAGGAAGTTTAATTCTCATGAGTAAGTGAAGGAAACTGCA
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAACAGTTGGCATGCCGTGAAGGT
GTTGGAAATAATTATGGATAAGAATAGCTCAATTATCCCAAATAATGGATGAAGCTATAA
TAGTTGGGAAAAGATTCTCAATGTTAAAGTCTAGAACAAAAGAATTCTTGAATA
AAAATATTATATAAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYEAGKIQKGREL
VGPFPGNLMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTTSNMTLRLRDRDFPWTTLMSLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGLAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFFEILDKLLDGDLTSDPSYFQNVTG
CSNNYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVEKYLREDTVQSVKPWL
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCCGGCTCCGAATGGCACATGTGGGATCCCACTCTTGTGGCTACAAACAT
TTTCCTCTTAACAAGCTAACAGCTGTTCAACAGCTAGTGATCAGGGTTCTCTTGC
GCTGGAGAAGAAGGGCTGAGGGCAGACGAGGGCACTCTACTCAGGGTACCCAGCTCTTG
CCTCTGTTGATAACAGACATGAGAAAGTGAAAGAGATGAGCGGAGTGAGGTGATGAAAG
TCTAAAATAGGAAGGAATTGTTGTCATAATCAGACTCTGGGAGGAGCTTGCACCTGGAGGC
CTGGGGAGGGCTGCCAACAGCTTCAAAACAGGAGGAGCTTCAACTGGGCTGGGAT
AAGACGTGCGGTAGGATAGGAAGACTGGGTTAGTCTTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAACAGATGGCTTAAGGGGCCAGAAA
TAGAGATGTTGAAATAAATTTAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
GAAAAACCAAATGAGGAAGGGAGGAGACTCACAGAGCTAACCCAGGATGGGACCCCTGGTC
AGGGCAGCCTTTGCTCTCCCGGAAATTATTTGCTGACCAACTCTGCCCCTGGTTT
GCAGAACATCATGTGAGGGCAACCGGGAGGTGGAGCAGATGAGCACACAGGAGCGCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGGCCCTGGCCCCGGGCGTGGAGGTGG
ACAGCGCTGTGCTGCTCATGAGTGGCTGGGAGCTGGGCCCCCAGCACCCGGC
ATGCTCATGTTGAGCACCTTCAACTCTGAGAACATGACTGACCTAACACTTACCGT
CCACCAAGGGACGGGGCGCTATGTGGGGCATCAACGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGCTCATAAAGCACGGGAGAACAGGACAAACAGTCTCGTACCCG
CCCTCATCTGCAGCCCTGAGGGAGCTCACCCTCACCAACAAATGTCACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCTGTGGCTGTGGAGGCTTACCCAGGGGCTGTGCA
AGCTGCTGCGCTGGATGACCTCTCATCTGTGGAGCCATCCACAAAGAGGAGCACTAC
CTGTCAGTGTCAACAAGACGGGACCATGTACGGGGTATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGGCTCTCATCGCACGGCTGTGGAGGGAGCAGATTACTTCCCGACCCCTGTC
GCCGGAAAGCTGCCCGAGACCCCTGAGTCTCAGGCCATGCTGACTATGAGCTACACAGC
ATTGTCATCTCATCGGCTTGCTAGTGGGGCTTGTCTACTTCTACTGTCCACGGGCG
CTTCTACATCTCATCGGCTTGCTAGTGGGGCTTGTCTACTTCTACTGTCCACGGGCG
CCCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTCTACACCTCACGCATCG
CTCTCGAAGGATGACCCCAAGTCCACTCATCGTGTCTGCCCTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCTCGCAGGCTGCTTACCTGGCAAGGCTGGGACTCTGGCC
AGGCTCTCAATATCACCGAGGAGCAGATGACTCTTGTGCTGTGCTTCCCTATCGGG
CAGTATCACCAACCGCCCGATGACTCTGCTGTGCTGTGCTTCCCTATCGGG
GCAGATCAAGGAGGAGCCCTGAGCTCTGTACCCAGGGGAGGGCAACCTGGAGCTCAACTGG
TGCTGGGGAGGAGCTCAGTCAGCACGAAGGGCCCTGTCCCCATCGATGATAACTCTGTG
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCTCTGACACCCAC
CAGCAGGGACCCATGACCTCTGTGGCTCTACGTTTACAACGGCTACAGCGTGGTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTCACTCTCATGAAAGACTCCCTTGTGAGGTAGCTATTGTGAGGATTTAACATAG
GCAACTTATTTCTTGTGGGAACAAAGGTAAATGGGGAGGTAAGAAGGGTTAATTGTG
ACTTAGCTCTAGCTACTCTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCTAAACTTTAAGAAAAACTTAAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLLQASLFAPPGNFWSDHSALCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP
RALEVDSDRSVLLSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLLDILFILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY
PPTLSSRKLPKDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFAASGGFVYFL
TVQQPETPEGVAINSAGDLFYTSRIVRLCKDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLGLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGGCCGGCTGAGTGGACTGGAGTGGGACCCGGGTCGGCGCTTAGAGAACACGCCATGCCA
CGTGGAGCCTCCGGCGAGGCCGCCACGCTGGACTCTCTCTGTGCTCTGGGCTTCCTGGCTGC
GCAGGCTGGACTGGAGCACCTGGATCTTCGGGGCTCCACAGACAGCTGGGCTGAGGCCAACGGCTGGA
ACTCTCATCTGGAGATTCAACCTCTGGATCTTCGGGGCTCCACACTTCTGGTGGACACCCCTACCCACTATTTCTGGTGGACAGGGACT
GGAGGGACCCGCTGCTGAGATGAAGGGCTGTGGCTTGAGAACACCCCTACCCACTATTTCTGGTGGACACCCCTACCCACTATTTCTGGTGGACAGGGACT
AGCCAGAAAGGCCAAATTGACTCTCTGGGACCTGGGACCTGGAGAACACCCCTACCCACTATTTCTGGTGGACAGGGACT
GGCTGTGGGTGATTCTGGCTCAGGGCCCCATACATCTGCACTGGAGATGGACCTCGGGGCTTCGCCAGCTGGCTAC
TCCAAGAACCTCTGGCATGAGGCTGAGGGACTGGGACCTGGAGAACACCCCTACCCAGGACTGGGACCTTATTTGACCA
TGATGTCAGGGTGGTGCACCTCAGTACAAGGGCTGGGACCTATCTGGCTGCAAGGGACTGGAGGACCTGGGCTTCCTG
CTCTGACTTCAGAACACAGGATGGGCTGAGAACAGGGGATTGTCAGGGGACTCTGGCACCACATCAACTCTGGAGT
CAACACAGGAGCTGCACTGAGTACAGCACCCCTTCCTCACTCAAGGCTGGGACCTGGAGGACCTGGGCTTCCTG
ACTGGGAGCTGGGTTGACTCTGGGAGCCCTACAAATCTGGGACTTCTGGGACCTTAACTTGGGCTTCATGAATG
CTGGGACTTCAGGGGCTCCATCACCTCTGGGACTTCTGGGACTTCAGGGGACTTCAGGGGACTTCAGGGG
GAGGGACTTCAGGGGACTTCAGGGGACTTCAGGGGACTTCAGGGGACTTCAGGGGACTTCAGGGG
ATTACACGGGCAACTGACATCTGGAGACTCTGGGACTTCAGGGGACTTCAGGGGACTTCAGGGG
ACCTCTCTCCAGATGGCGTATGAGCCCCTAACGGGAGACTTCAGGGGACTTCAGGGGACTTCAGGGG
TGGGGGAGCCAAATCAAGTCTGAGAACAGGACATCACTGGGAGGAAATGGGAGGAAATGGGAGCT
TCAGGGTACATTCTCATGAGACCAACATCTGGGACTTCAGGGGACTTCAGGGGACTTCAGGGG
TGTTTGTGAACACAGTATCTGAGATTCTGGGACTACAGAACACAGAAGATTCTGTCCCCCTGATCAGGGTT
ACATGGGAGCTGGGGATCTTGAGGAATCTGGGAGGACTTCAGGGGAGACTTCAGGGGACTTCAGGG
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAATCTGAGATCTATGCTGGGATATGAAAGAAG
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAATCTGAGATCTATGCTGGGATATGAAAGAAG
CTCTCTTCTGAGGGTGGCCCTGGACAAATTGGGAGCTCCGGGACAAACCCACATTACTGGCTTTCTCTGG
GTAGCTTCTGCTCATGCTCCA CGGGCTGTGAGACCTTCTGAGCTGGAGGGCTGGGAGAAGGGGTTGATTCA
TCATGGGCAACACTGGGACTTCAGGGGACTTCAGGGGACTTCAGGGGACTTCAGGGG
GCACGGGAATCAACCGAGTCTGGGAGGACTTCAGGGGACTTCAGGGGACTTCAGGG
ACCTGGGAGGAACCCAGTACATTAGTGGAGCTGGGAGGACTTCAGGGGACTTCAGGG
CTCTTGAGCTGGGACTTCAGGGGACTTCAGGGGACTTCAGGGGACTTCAGGG
ACTGGGGGACTTCAGGGGACTTCAGGGGACTTCAGGGGACTTCAGGG
TGGCTTGTGATGCTCTTCTACAGGCTCTGGGCTCTGGGAGGACTTCAGGGGACTTCAGGG
AGCTTAATCATGATGGCCAGCCTTGGGCTCTGGGAGGACTTCAGGGGACTTCAGGG
TGGCAGGACTCTGCTGACTCAGGGCTCTTGTGGTCTCTGGGAGGACTTCAGGG
TTTATCCCCGAAATCTGGGTGTGTCACAGATGTAGAGGGTGGGGAGGGGACTTCAGGG
CTTCTCTTCTACAAACCTCTGAGCTCTTGGGATTCTGGGAGGACTTCAGGG
TCCCTTCCACTCTCTCTGGGCTCTGGGAGGACTTCAGGGGACTTCAGGG
CAAGTAGCAGGTGTTCTGTGTTCTGAGCTGGAGGACATGTGAGTCTGGCAGAACGG
CATTCAGGGAGGGAGGGACAGAAGGGCCAGCTCACATGTGAGTCTGGCAGAACGG
AGGGAGGGAGGACAGAAGGGCCAGCTCACATGTGAGTCTGGCAGAACGG
GGAGGGACAGAGGGCCAGCTCACATGTGAGTCTGGCAGAACGG
ACAGAAGGGCCAGCTAGTGGCCCCGCTCCCAACCCCCCAAGCCGAACAGCAGGG
GAAGTGTGTCACATGGGCTTGTGAGGCTTGTCTGGGCCCCAGCCAAACCTGGCTTGGGCTCACTGTCTGG
GTTGAGTAAAGCTATAACACCTGAACTCACAA

FIGURE 64

MTTWSLRRRPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLQDPMRLLRTTYKGFTEAVIDLYFDHLMRSRVVPLQ
YKRGGPIAVQVENEYGSYNKDPAVMPPVKKALEDRGIVELLLLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVMEMYWTGWFDSWGGPHNILDsseVLKTVSAIVDAGS
SINLYMFHGCTNFGFMNGAMHFHDYKSDVTSYDYDAVLTTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNNGNGQSFYIYE
TSITSSGILSGHVHDRVQVFVNTVSIGFLDYKTTKIAVPLIQGYTVLRLVNRGRVNYGEN
IDDQRKGLIGNLYLNDSPLKNFRIYSLDMKKSFFQRFGLDKWXSLPPTPLPAFFLGLSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGTAGCTAGGTAGGGTGGACGGTCCAGGACC
CTGGTAGGGTTCTACTTGGCCTCGGTGGGGTCAGAGCGCAGCACCTACGCCAAGG
GGAGCAAAAGCCGGCTCGGCCGAGGCCCAAGGCCTCCATCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGCGGCTCAGACTAGAGGAGGGCTGTAAACGCC**ATGGCTCC**
AAAGAGCTGTCTGCCCTCGTCCCTGCTGACGGCTACGCCACTGCTGAGGCC
GGCAGACACTCGGTGTTCTGAGTGATAGGGTCATGACGGTTCTCTAGACGGGCC
CGTTCGCGTATGTTGCTGCGCAGCTGCACTATTCCGGTACCGCGGGTCTTGCGAC
CGGCTTTGAGAGATGCGATGGCGCCCAACGCCATACAGTTATGTCCTGGGAACTA
CCACGAGGCCACAGCCCTGGGTCTATACTTAACTTAACTGGCAGCGGGACCTCAT
ATGAGGCAGCTCTAGGAACCTGTGGTCATACTGAGAACAGGACCTACATCTGTGAGAG
TGGGAGATGGGGGGTCTCCATCTGGTCTGGAAAACCTCATCTAAAGAACCTC
AGATCCAGACTCTTCCGCGCAGTGGACTCTGGTCAAGGCTTGCTGCCAAGATATAC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATA
TACAGAGCGCTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTTGGCTCTTACACAGATGGGGCTGAAGGACTCAAGTGTGGCTCCCGGG
GACTCTATAACCACTGTAGATTGGCCCGCTGACAAACATGACCAAATCTTACCTGCTT
CGGAAGATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGGCCAGATCACTCCACAGCTGTGAGCTGTAACCCAAAGGACTAGAGAACATGC
TCAAGTGGGAGGCCAGTGTGAAACATGTACATGTTCCATGGAGGTACCAACTTGGATTATGG
AATGGTGCGATAAGAAGGGAGCCTCCCTCGATTACTACAGCTATGACTATGATGC
TATATCTGAAGCAGGGGACCCACACCTAACGGTTTGCTCTTCGAGATGT
CATGACAGT TCCAGGAAGTCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCCCTAGACTTGTGCTTGGCCCCGTGGCCCCAT
TCATTCAATCTTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC
GAACCTATATGACCCATACATTGGAGCCAACACCATCTGGGTGCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGGTGTCCAGGGTGTGAGC
AGACAAACTATTTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGTCTAACAGCAGTACTTCAGGGCTGTGAGGCCACCAATTCTG
GGCCAACAAACTCTTACCCAGTGGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTTCCCTCCAGTGGCAAATGGGATATCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAAATTAGGCTCAGTGGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACTTGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCTCTACGTGCCAAGATTCTCTGTTCTAGGGGACCCCTAACAAAATTAA
CATTGCTGGAACTAGAAGATGTACCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCAGTACTTGCACAGGACACATATCAATTCCCTTCTGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAAGTGGGCAC**TGAAAGGTAGGCCGGCATGGTGGCTCATGC**
CTGTAATCCAGCATTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGACTTCAAGA
CCAGCCTGCCAACATGGTGAACCCCGTCTCAACTAAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAAATCCAGTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGAGGAGGTTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTAAAAAAAAAA

FIGURE 66

MAPKKLSCRSLLLPLSLTLLPQADTRSFVVDRGHDRLFLDGA
FPRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYWPWNYHEPQPGVYNFGNSRDLIAFLNEA
ALANLLVILRPGPYI
CAEWEMGGGLPSWLRLKPEIHLRTSDPDFLA
AVDSWFKVLLPKIYPWLYHNGGN
ISIQVE
YGSYRACDFSYMRHLAGLFRA
LLGEKILLFTTDGPEGLKCGSLRG
LYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWL
DYWGQNHS
TRSVSAVTKGLENMLKL
GASVNMYMFHGGTNF
GYWNGADKKGRFLP
ITTSYDYDAP
ISEAGDPTPKLFA
LRDVISKFQE
VPLGPLPPPSPKM
ML
GPVTLHLVGHL
LLAFLD
LLCPRG
PIHSI
LPMTFE
A
VKQDHG
FMLYRTY
MHTI
FEPT
PFWVPN
NGVHDRAYVM
VDGVFQGV
VERNMRDKL
FLTGK
LGSKLD
DILVEN
MGRLSFG
NSDF
KG
LLP
P
ILGQ
TILTQWM
MFPLK
IDNLV
KWWFPL
QLPKW
PYQP
APSG
PTFY
SKTF
P
ILGS
VGDT
FLY
L
PGWT
KGQV
WING
FN
NL
GRY
WT
KQGP
QQTL
YV
P
R
F
P
R
G
A
LN
K
IT
L
LE
E
D
V
P
L
Q
P
Q
V
Q
F
L
D
K
P
I
L
N
S
T
L
H
R
T
H
I
N
S
L
A
D
T
L
S
A
S
E
P
M
E
L
S
G
H

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAAACAGTCTGCAAGCCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTG
ACCCACAATATGGCTTACATGTTGAAAAGCTTCTCATCAGTTACATATCATTATTGTGT
TTATGGCTTATCTGCCTCACACTCTCTGGTTATCAGGATACCTTGAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCCAGATGTCAAAAGATTT
GCGTTCTCTTCACATGGTAGACAGTATGACCAGCTATATTCCAAGCCTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAGAAATAAACTTAGGAAATTAGTGTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTCAACAGCCCAGGACAAGCAGGAGTTGCATCTGTCATG
CTGTCGGGGTGCCGATGCTCTTGACCTCACAGACCTGGATGTGCTAAAGCTGAACT
AATTCCAGAACGCTAAATTCTGCTAAGATTCTCAATGACTAACCTCCAAGGCTCCACC
CTGCCACTGCCCTGCAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCATTGAGA
TGCCCTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCCTGGGTGATTGCTCAAAA
CCTTCGAGAGGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCGAGAGGTTGCGGCCACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAATTACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCCACAATTGAGGAATCATGAGCTTCCACGCTTAAACGACT
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTTATTACCCATGTCA
AAAACTGGAGTCACTTTATTCTCTAACACAAGCTGAATCCTTACAGTGGCAGTATT
AGTTTACAGAAAACCTCAGATGCTTAGATGTGAGCTACAACACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCACTGGCATATCAGTGGAAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCATAAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCCTGCCAGGCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCAGGCTTGGT
TGGAAAGATCACCTTTTGATACCTGCCACTCGAAGTCAAAGAGGATTGAATCAAGACATA
AATATTCCCTTGCAATGGATTAAACTAAGATAATATATGACACAGTGTGCAAGAAC
AACTCCCTAGATTGCAAGTGCCTACGTACAAGTTTACAAGATAATGCATTAGGAGTAG
ATACATCTTAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTAAGTCATTCAATTCCAAATCATTGTTTTCTTTGGGG
AAAGGGAAAGGAAAATTATAATCAACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPPLKEYSFEKVREESSFSDI PDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEI PAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVHNDGTKLVLNSLKKMMNVAEELQNCALERI PHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLLTCKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSPL
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRLMKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

FIGURE 70

MELVRRLLMPLTLLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPESENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPPLLGVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVYFFFSPNISIPNCGGYLDTLLEGSGFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNLNKEIFLEDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIYIYTEDDVIQSQNALKYNTSMALFESNSFEKTILESPYYVVDLNQTLFVQVSLHTSDPN
LUVFLDTCRASPSTDFASTPYDLIKSGCSRDETCKVYPLFGHYGRFQFNAKFLRSMSSSVYL
QCKVLICDSSDHQSRCNQGCCVSRSKRDISSYKWKTDSIIGPIRLKRDRSASGNQFCQHETHA
ETTPNQPFNSVHLFSFMVLALNVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGGAGCCTGCAGAGAGGACAGCGGCTGCAGC
GGACATGCGCCCCAGGAGCTCCCAAGGCTCGCTTCCCGTTGCTCTGTTGCTGTGCTC
TGCTGCCGCCGCCGCGCTGCCCTGCCACAGCGCACCGCCTCGACCCCACCTGGGAGTC
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCCAGGCAAGTTCGCATCTTCATCCACTG
GGGACTGTTTCCGTCGCCAGCTTCCGGTAGCGACTGGTTCTGGTGTATTGGCAAAGGAAA
AGATAACCGAAGTATGAAATTATGAAAGATAATTACCCCTCACTGTTCAAATATGAAGAT
TTTGGACCACATTTACAGAAAATTTTAATGCCAACAGTGGGAGCATTTTCAGGC
CTCTGGTCCAAATACATTGCTTAACTTCAACATCATGAAAGGCTTACCTTGTGGGGGT
CAGAATAATTCTGGAACGTGAACTGCAATGATGAGGGCCAAGAGGGACATTGCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTGGACTGTACTATTCCCTTTGA
ATGGTTTACCCGCTCTCCCTGAGGATGAATCCAGTTCAATTCCATAAGCGGAATTTCAG
TTCTAAAGACATTGCCAGGAGCTCTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGCTGAGGGAGCACGGGATCAAATCTGAAACAGCACAGCTTCTGGCTGGTT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGCCTCTATACTCGTAGTCAGTCAATGGAGAACATTTGGCCA
CATAAATGGGAAACTCTGATGACAATAGAACACTGCTCTGGGCTATAGGAGGAAGCTGG
ATATCTGACTATCTAACATTGAAGAAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTTGTGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGTAG
GAGCAGCTGGAGCAAGTGGGTCTGGCTAAAGTCATGGAGAACATTTATGAAACCTA
TACCTGGCGATCCCGAAATGACACTGTCACCCAGATGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTCCTAAATGGCCACATCAGGACAGCTGTTCCCTGGCCAT
CCCAAAACTTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAATCG
GATTTCCTTGGAGCAAATGGCATTATGGTAGAACATGCCAACAGCTAACCATTCAGATGC
CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATTCAGGTGTCATAATTGTAGCAATGGAGA
AAGCAATGTAACCTGGATAAGAAAATTATTGGCAGTTAGCCCTTCCCTTTCCCACTA
AATTTCCTTAAATTACCCATGTAAACCATTTTAACTCTCAGTCACATTGCAATTAAAGTC
TCTTCACATTGATTTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAAACTGAAAATTTTATGGTAAGGCCATATCCCCCATG
ATTATATAGTTATGCACTAACATTGGGATATTTCCTGGGAATGCAATTGCTAGTCAT
TTTTTTTGTGCCACATCATAGAGTGTATTACAAATCCTAGATGGCATAGCCTACTACA
CACCTAACTGTGATGTTAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATGGTCACCTGTATAGGGCACTTACCCAGAATGGAG
CTTACAGGACTGGAGTTGCTCGGGTGAAGTCAGTGAATGTGAAGGCCATGGACATTA
TTGAACACTGCCCAGACGTTAAATAAACTGTGTTAGCTTGGCTACACTACATTATAAAAAAA
GTTTTCTTCTCAATTATAAAATTACATAAGTGTACTGTAACTTACAAACGTTAAATT
TTTAAACCTTTGGCTTTGTAAATAACACTTAGCTTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFLPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG
VFSVPSFGSEWFWWYWKKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWAGSICKHGGFYTCSDRYNPGLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIIGPTLDGTISVVFEERLRQVGSQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGATGTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCTAACATAGT
TCCAGAACTCTCATCCGACTAGTTATTGAGCATCTGCCCTCATATCACCGTGCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCTGGTGTG
CTTCACTTCACTGGACACGAGGCTCTGGTCCAAGGCTTCTGGCTGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAAATTATGGATCACCTTGTGAGCAAAAGCGAACAGC
AGCTGAATTACAGAAGCTAAGGAGGCCGTAGGCTGCTGGGACTAAGTTGGCCGGCAAG
GACCAAGTGAACAGCCTGAAAGCTAGCTTGAACACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTCACTCTAGGTAGCTTGAACAGGCAAGCTTGCAGCTATTGTACACTCATCTGAT
TCCTGATTGGAGGGTCCAGTGAGCCGACAGTTTGAGCCTATTGTACACTCATCTGAT
ACTTGGACTAAGCTGCACTCCAGAAATTATCACCAACAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAACAGAATTATTGAGCTGAGTGCAGTACCTACTCGGTGCACTCCCTT
ACTCTACAATACCTGCCCTACTACTACTCTCTGCCAGCTTCACTTCTATTCCACCG
AGAAAAAAATTGATTGTCAGAAAGTTTATGAAACTAGCACATGTCTACAGAAC
TGAACATTGTTGAAATAAGCAGCATTCAAGAATGAGCTGCTGGGTTGGAGGTGTC
CCACGGCTCTGCTAGTGCCTCTCTTGTGCTGCAGCTGGTGGATTGTC
TATGTCAAAAGGTATGTAAGGCTTCTCCCTTACAAACAAAGATCAGCAGAAGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAACAGTCCAAGGCTCAAGGAAACACTACCGTGCATGCTGAA
GCTGAAGTTAGTGAGACAGAAATGAGGAGACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCCGACGTTGGAAATCAAAGGCCAAAGAACCAAAGAACAGTCCACCTT
GGTTCTTACTGGAATCAGCTCAGGACTGCCATTGACTATGGAGTGCAACAAAGAGAACATGC
CCTTCTCTTATGTAACCTGCTGGATCTTACCTCTTACCTCCAAAGCTTCCACGCC
TTTCTAGCTGGCTATGCTCTAAATAATCTCCACTGGGAAAGGAGTTTGCACAGGCAA
GGACCTAAACATCTCATCAGTATCAGTGGTAAAAGGCCCTCTGGCTGCTGAGGCTAGG
TGGGTTGAAAGCCAAGGACTACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGAC
CCTTCTCTCAGCTGAAAGGAAACAGCTATGCCACCTGACATGCTCTGAGCCCCGTA
AGACCAAAGAATGCGAGAAAAGTTAGCCCTGAAAGGCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGAAAGCTAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGCTAAAGGTGTTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGCTCTACCACTGCTGATATTCT
AGGAATATACTTTACAAGTAACAAAATAAAACTCTTATAATTCTTATTTTATCTGA
GTTACAGAAATGTTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATGTCAGGCTGCTGCAAGCTTACACTCTGTAAT
TGAATTATTCTCTAAAAATTGCACTAGTAGAACGCTATCTGGAAAGCTATTCT
GTTTGTGATATTCTAGCTTACTCTTCCAAACTAATTCTTATTCTGAGACTAATCTT
ATTCTATTCTCTAATATGGCAACCACTTAAACCTTAAATTAAACATACCTAAGAAG
TACATTGTTACCTCTATATAACCAAGCACATTAAAAGTGCCATTAAACATGTATCACTA
GCCCTCTTTCCAACAAGAAGGGACTGAGAGATGCGAGAAATATTGTGACAAAAAATTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLLTSIWTTTRLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFTPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTCGGTGCCTGACTTTCAAGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGA
ACTGCCGCCCTGCCACGGCTGCCACCCAACGCGAACAGCGTAACCGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTCCGTTGGATATTGCGATGGCCTACTTACATCACACTGCGATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACCTAGAACGGACAAGAGGGTCACTGGATTGGAGTTCTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGGAAGGGTGGATGTTGGACGCTACTGATGTTAGTACCGGTAC
AAAGTGGACACATCACCCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGTGTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACAGCGGGCAAGAAACTATCA
AAGGCTGGAGACAATATCCTGAGGAGCAGCCTGCGCTCAACCCCCACAGTGTCA
TGGGGAAAACAAGAAGGATAAATAGATCCTCACTTTGGAGTGCCTCTCTCTGTC
CCAGGCTCTTCCATAACCCAAGCCTGAGGCTGCAGCCTTNAATTNATGTTTCCCTTG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGCTGCCATGCTGGCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCAAGCTGGTCAGTGTGTTAATGCTTATC
AGCTATTGACACATCTCCATGGTTCTCCATGAAACTCTGTTGTTCATCATTCTCTTAG
TTGACCTGCAAGCTGGTTAGACCTAGTTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCTTCAAGGACTCTGCTCCCTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCTAACCTTGTGCGTAGTCCTAAGGAGAAACCTTAAACCAAAAG
TTTTTATCATTGAAAGACAATATTGAAACAACCCCCCTATTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTGAGACTTCCCTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCA
TAACCCCTGACATACTCCCCAACCCAGTTGATGGCTTCCGTAATAAAAGATTGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSPVRLSRWLAQPYYLALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRDLIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSF APIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPPEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYNSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPPRRVRVKWWKLSENGAAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRRAWEEGLDWNCAGWLQDATVQYPIMLPQPCGGPGLAPGVRSYGR
HRRRLHRYDVFCFATALKGRRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

FIGURE 80

MMWRPSVLLLRLHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDRGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHLDGSEVGHVLPQAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCCTTGCCTTCGCACTCGGGCGCAGCGGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
CGGGCGGGCGGGTGCAGGGATCCCTGACGCCCTGTTCTGACCCAGACAGCTAGAGGGGGCGTGGCCTGAGCAG
CCTGTCGTCGTCGTTGGCGCCCCCGCTCCCGCCGGTGCAGGGGGTGACACCCGATCTG
GGCTTCGCTCGATTTCGCCGGCGCCTCCCGAGACAGCTAGAGGGGGCGTGGCCTGAGCAG
CGGGTCTGCTGTTCTCTCTGCGCCGCCGGGGATCCGAAGGGTGCGGGCTCT
GAGGAGGTGACGCCGGGCTCCGCACCCCTGGCCATTCTCCCTCTCCAG
GTGTGAGCACGCTATCAGTCACCATGTCGAGCCTGAGATCCCGCTCTGGCCCTGGTGTG
TGTCTGCTGCTGCTGCCGGGGCGGGAGCGAGGGAGGGAGGGAGGGCTCCATTGCTATCACATG
TTTACACAGGGCTTGGACATCAGGAAGGAAAGCAGATGTCTCTGCCCAGGGGCTGCC
CTCTTGAGGAATTCTGTTGATGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGGAAATCAGCAACTCAGGGGACCTGACAGTCTATAGCCTACC
TGGCTGAGAAAACATTCTCAGTATGGCATTCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCAGTAACAAAGGAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACAAAGGTAACAGCTAAAGAAAACACCCGAGAAGAAAACCTGG
CAATAAAAGATTGTAAGCAGACATTCGATCTTCTGATTGATGGAAAGCTTAAATTGGGAGC
GCCGATTAAATTTCAGAAGAATTGGTGTGAAAAGTGTCTTAATGTTGGGAAATTGGGAA
GAAGGACCATGTTGGGCTTCAAGGAGTGAACATCCAAAATAGAATTTCATTGAA
AAACTTACATCAGGAAAGATGTTTGTGCTTCAAGGAGTGAACATCCAAAATAGAATTTCATTGAA
ATTCCAATACAGGAAAGGCCATTGAGCATACTGTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGATCCCAACTGGTGTGTTATTATGGATGGTGCCTGATGACAT
CGAGGAAGCAGGATTGTGCCAGAGAGTTGGTGTCAATGTTAGTTCATTGTTCTGGCCA
AGCCTATCCCTGAAAGACTGGGATGGTCAAGGCTGACATTGTTGACAAGGCTGCTGT
CGGAAATAGGCTTCTCTTCTACATGCCAACCTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGCACTCATGAAACAAATGATGTCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCCTTCAATTGATGGCTCAGCAGTGGGAGATGCAATTTCGCCCTC
ATGCTGAAATTGGTTCACATGCAAGACTTTGAAATCTGGACATTGGTGCCAAGAT
AGCTGCTGACAGTTACTTATGATCAGGCCACGGAGTCAGTTCACTGACTATAGCACCA
AAGAGAATGCTCTAGCTGTCATCAGAAACATCGCTATAAGTGGTGGAACAGCTACTGGT
GATGCCATTTCCTTCACTGGTAGAAAATGTTGGGCCATAAGGGAGGCCAACAGAA
CTTCTCTAGTAATTGTCACAGATGGCAGTCATGATGATGTCAGGCTTCTGGATGACCTG
CACATGATGCCAGGAATCACTATCTCTGTTGGTGTGGCTTGGCACCCTGGAATTGACCTG
AAAGATATGGCTTCAAAACCGAAGGGACTCACGCTTCTTCAAAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCAATTGAGATTTCTAGAATCCAGCAAT
AATGGTAACTTTGACAACAGGAAAGAAAGTACAAGGGATCCAGTGTGAAATTGATT
CTCATAACTGAAATGCTTACAGTACAGTACAAACTTAAAGTATGTCAC
AGCCATTAGGCAAAATAAGCCTTAAAGCCGCTGCCATTCTGGTTACAATTTCAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATGCGCTTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTCTAACCATGCCACTAAATGTACAGATATGCAA
TTCCATAGCTCAAAAAAGAATCTGATACTTAGACCAAAAAAAAAAA

FIGURE 82

M S A A W I P A L G L G V C L L L P P G P A G S E G A A P I A I T C F T R G L D I R K E A D V L C P G G C P L E E F S V Y
G N I V Y A S V S S I C G A A V H R G V I S N S G G P V R V Y S L P G R E N Y S S V D A N G I Q S Q M L S R W S A S F T V T
K G K S S T Q E A T G Q A V S T A H P P T G K R L K K T P E K K T G N K D C K A D I A F L I D G S F N I G Q R R F N L Q K N
F V G K V A L M L G I G T E G P H V G L V Q A S E H P K I E F Y L K N F T S A K D V L F A I K E V G F R G G N S N T G K A L
K H T A Q K F F T V D A G V R K G I P K V V V V F I D G W P S D D I E E A G I V A R E F G V N V F I V S V A K P I P E E L G
M V Q D V T F V D K A V C R N N G F F S Y H M P N W F G T T K Y V K P L V Q K L C T H E Q M M C S K T C Y N S V N I A F L I
D G S S V G D S N F R L M L E F V S N I A K T F E I S D I G A K I A A V Q F T Y D Q R T E F S F T D Y S T K E N V L A V I
R N I R Y M S G G T A T G D A I S F T V R N V F G P I R E S P N K N F L V I V T D G Q S Y D D V Q G P A A A H D A G I T I
F S V G V A W A P L D D L K D M A S K P K E S H A F F T R E F T G L E P I V S D V I R G I C R D F L E S Q Q

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGGCGTCCCGCACCCGGGCCCCACCGCGCCGCTCCGCATCTGACCCCGAGGCC
GGCGGCTCCCGGGAGCAGATCCAGTCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGCGCGGCGCTCGGGCGCAGAGCGGAGAT**TCG**CAGCGGCTGGGGCACCCCTGCTGCGCTG
TGCTGGGGCGGGCTCCACGGGCCCCCGCGCTCGAGCGGACCTCGGTCCAGTC
AAGCCGGGCCCCCTCTCACGGGCGAGGAGCCACCCCTCAATGAGATGTTCCGCGA
GGTTAGGAACTGATGGAGGACAGCAGCACAAATTGGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT
CACAATGAGACCAACACAGACACAGAAGGGTGGAAATAATACCATCCATGTGCAACCGAGAAAT
TCACAGATAACCAACACAGACTGGACAAATGGTCTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGAGCCAGAGTGCATCATCGACGAGGACTGTGGGGCCAGC
ATGTAAGTGGCAGTGGCAGCTTCCAGTACACCTGCGCACCCATGCGGGGAGGAGATGCT
CTGCACCCGGGAGCAGTGTGGAGGACAGCTGTGTCTGGGGTCACTGCAACAAA
TGGGCCACCGAGGGCAGCAATGGGACCATCTGTGACAACCCAGGGACTGCCACCGGGGCTG
TGCTGTGCCTCCAGAGAGGCCAGCTGTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA
GCTTGGCCATGACCCGGCAGGGCTCTGAGACCTCACCTGGAGACTAGAGCTGTGATG
GAGGCTTGGACCATGGCTTGTGCACTGGCCACAGCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCTGCTGCC
CAGAGAGGTCCCCAGTGAAGTGAAGTTGGCAGCTTCATGGAGGAGCTGCCAGGAGCTGG
AGGACCTGGAGGGAGGCGTACTGAGAGATGGCGTGGGGAGCCTGGGCTGCCCGCT
GCACTGTGGAGGGAGGAT**TAG**ATGGGACAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTTCCCAGGTGTGCTTAGGGTGTGGCTGACCAGGCTTCTCTACA
TCTTCTCCAGTAAGTTCCTCTGGCTGACAGCATGGGTGTTGCAATTGTTCTACG
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTGTGGCTGGAGACTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCACTGGCTTGTGAAATTGTTGGGGAGGAGATGGAAACATGTGG
ACAGCCCTTGTCTACATGGCTTGTGAAATTGTTGGGGAGGAGATGGAAACATGTGG
AGTCTCCTCTGTGTTGGGGAAATGTGAGGGAGGAGATGGCAAAACATGTCAA
CTGGGAAATATGCAACAAATGAATTCTCACGGCAGTTCTTCCATGGGATAGTAAAGCTG
TGCCCTCAGCTGTGAGATGAAATGTTGTTCACCTGCATTACATGTGTTATTCACTCC
AGCAGTGTGCTCAGCTCCACCTCTGTGCGAGGAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCTCGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCT
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGGTGCACCAA
AAGTGTCTCCAAAAGGAAGGAGAATGGGATTTCTGGGGCATGCACATCTGGAAATTAAG
GTCAAATTAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAAACAGCAGTGTCTCAC
AGTGTGGGCAGCGTCCCTCTAATGAAGACAATGATATTGACACTGTCCCTTGGGAGT
TGCAATTAGTAACCTTGAAAAGGTATATGACTGAGCGTACAGGTTAACCTGCAGAAACA
GTACTTTAGGTAATTGAGGGCAGGATTAAATGAAATTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACTGGAGAAAATCAAACCGAGCAGGGTGTGAAACATGGT
GTAATATGCGAACTCGGAACACTGCAACTACGCCACTCACAAATGATGTTTCACTGGTCA
TGGACTGTGGCCACCATGTATTCTCACGGAGTTCTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGTGAGTTAAATTATGATATAACATAAGTGCATTTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSVVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEEMAEAAAAKASSEVNLANLPPSYHNETNTDKVGNNNTIHVHREIHKITNNQTG
QMVFSETVTISVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSSECG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEIILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAGAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATTAATTCAGCCCATCCACTCTCTTCCCTCAGAACACATGTGCAGTGCACACACACATACA
CACACATACACCTCTCCCTCAGAACACTGCAGACTCAGACTCAGCTCTGGCAGCAGGTCAAGAAAGGACAC
TAAAGCCTTAAGGCAGGGCTGGGATTACCTCTCAGCTCTTGGCTTGTGAGTCAAAAACATGGGAGGG
CGCAGGAGCTGGTCACTCAGCTTGGGAGGAAACCTGGCAGGAGGATCTGGGAGGAGGAGGAGGAGG
TTCGAGACGACCTGGGCCAACATGGAGAAAACCCCACATCTACTAATAAAATACAAAATTAGCCAGGAGTGGGC
AGGTGCCGTAACTCCACAGTCACTCAGGTGGCTGAGCCAGGAGAATCGCTGAATCCAGGAGGGAGATGCCAGT
CAGCTGAGTGCACCCGGCTGCACACTCTGGAGCAGACTGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
GGGGTAGATACTGCTCTCAGCAACTCTCTGGCATACTCTCTCTCAGGGCTGCCCTGTAGGGGCTG
GCAATGACTGAGCAGGGCCAACCCAGGAGGAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GTGAGAATGACTGCCCTGGGAGGGTTCTCTGGGCTCTGGCAGGGTGTGACCCCTAACCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCTGTGAGTGTCCCCTGCCCTGAGCTCACCACAGGCTTCTGGGCCCC
ACTCTCTGAGCTGGGTGCTGGCCACTGCCACAGTGCCCTGAGCTGACCTCTGGCTTACCTGGCTGTCTCTGGGCCCC
GTGTCCTGCCAGGATCCGGCTCTGGCTGAGAGACTCTGCTCAGGGCTGCCCTGAGCTACCCACTGTGGACTCTGCAATGA
CTCTTCTCTGGGAGG
CTGGTGTGGGAGG
TGCCCGAGACTGTGATTTCCATGCCCTGCCCTGAGCTGAGCTGCCACTAGGAGGAACCCAGCTGACCCGGCT
GGAGGGACACAGTGCCAGGGCTGGCAGGCTCACAGGAACCTCTGACCCCTAACACAGGCTCTACCCAGGCT
CCCCAGGGCTTCTCTGCCCTCACAACTTGCTGCCCTGAGCTAACACTCCAAACCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGG
CGCTGGTTGAATGCTGGCCAATCTGGAGATACATGATTTGGGGCAAACTGGAGATGCTGGGACATCTGGGACAT
GAACCTGGGCCGGCTGGGAACTCTGGTAGCTGGTAGCTGGAGGACTGAACACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GGAACCTGGGCCGGGGCTGGAAAGCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CAACATECTGCCACTTAAGGAGCTGGGAGTGAACACATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CTCTGGGAGGGCTGAAAGCTCTGGAGG
GAACTTCCCGGGAGCTGGGAGG
CCACCTGGGGAGGAGTGGAGG
CTCTGGGAGGGCTGGAGG
CACGGGGCCGGCTGGCTCTGGAGCGCAATCCACCCCTGTGAGCGGACTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GGTCTGGTGGGGCTGGCTGACTGACAGCTGCCACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GGTCACTGCCACTGGGCTGGCTGACTGACAGCTGCCACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GGAGCTGGGGAGGTTGAGAGG
TAAGAGCTTGTAGTGTGTTGTGGGGCTGCTCTCCCTCAGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GGTGCAGGGAGACCCACCCCTATCACATCTGCTATCTGGGTCACCCACCAACACAGTGTCCACCAACCTCAC
CTGGGCTGGAGCTCTCTCCCTGGGGGAGGGGGCAACAGCTGGGGCTGGCTGGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CAACATTCTACCCGGCTCTGGGGAGG
GTTGGCTTGTGTATGGGGCTGGGGAGG
TGCCATCTGGCTCTGGCTCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGG
GGTGTGGGGTGGAGGGGGCTCTCCCTCCAGGCTGGGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGG
GTCTGCTCCCCCTCTGGCTCTGGGGCTGGAGG
ACCATTTGCTCAAATTTCTGAGGCTCAGCTGGCTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACAAA
AGAGAAGCAGTCTGGGAGGAGTGGGGCTCCAGGAAAGGGACATGGAGGCCACAGTGTGGAGGGCTGGCACTGG
CAAGACAGATGGGGTTTGTGGGGCTGGCTCTGGAGCTTGTGGCTAGGCTTGTGGCTTACCTCTGGGGCT
CTCTGCTGGCATTCTGAGGAACTCTCAAGGAAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CTCTCTGCCAGAGGGCTCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGG
TCCTCTCTGTCAGTCTCAGTGTGCTCTCTGTGCTCTCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGGGCTGG
CTCGGGGGGGCTGCCCTAATGTGGGGAGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CGCCTCATCTCAGAGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG
ATGTGTACCTCCCCAACCCGATTCACTTTTCTCTGTTTGTAAAAAATAAAAATAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRDQSELGYLANLTELDSQNSFSDARDCDFHALPQLLSLHL
ERNQLTRLEDHSFAGLASIQLELYLHNQQLYRIAPRAFSGLSNLLRLLHNSNLLRAIDSRWFE
MLPNLIELMIGGNKVDAILDMNFRPLANLRSVLVAGMNLREISDYALEGLQSLSESLSFYDNQ
LARVPRRALEQVPGLKFDLNKNPLQRVGPGDFANMLLHKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLPKQMETLMLNNNALSAHQQTVESLPNLQEVLGHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPDPLQLRPVREVFREMTDHCLPLISRSPFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGDADTKTVSVVGRALLQPGRDEQOGLELRVQETHPYHILLSWTPPTVSTNLTW
SSASSLRGGGATALARLPRGTHSYNITRLLQATEYWAQVAFADAHTQIACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHHGTGQPRKGVGGRRLPAAFWGWSAPSVRVV
SAPLVLWPWNPGRKLPNSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

FIGURE 88

MRQTIIKVIKFILIIICYTVVYVHNIFKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRSLKKYSFESIREESSYSIDPVKNDFAFLHLHIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNNEWTLDKLRLQRLLTKNAQDKLELHLFMLS GIPDTVFDLVELEV
LKLELIPDVТИPPSIAQLTCLKEWLWLYHTAAKIEAPALAFLRENLRALHIKPTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVRLKSNL SKLPQVVTDVGVLQKLSI
NNEGTKLIVLNSLKKMANLTELLELIRCDLERIPH SIFSLSHNLQFIDLKDNNLKTIEIIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLALHGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGGTACTTGTCATGGAGCTGGCACTGCGCGCTCCCGT
CCC CGGTGGTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGT CATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGAAGGATGCCTACATG
TTCTGGTGCTCTATTATGCCACCAACTCCGTCAAGAACTTCTCAGAAGTGCCTGGTCAT
GTGGCCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAACTTGAGGAATTGGG
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCTATT
GTGGATAATCCC GTGGGACTGGGTCAGTTATGTGAATGGTAGTGGTGCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGAACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTAAGGCCATTCAAGCAGGGGACCATCAAGTGCACACTTGGGGGGT
TGCCTGGGTGATTCTGGATCTCCCTGGTATTGGTGCTCTCTGGGACCTAACCTGT
ACAGCATGTCCTTCTGAAGACAAAGGTCTGGCAGAGGTGTTCAAGGGTGCAGAGCAAGTA
CTGAATGCCGTTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTTGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACTAAAGCACTCCCC
CGTCTACAATGGAGTCGAGTCTAGAAATTCACACAGGCCACCTAGTTGTCTTGTCAAGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGCCACATCAGAAAGAA
GCTCAAATTATTCTGGAGGATCAATCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGGTGACGAGTTGGCTGGAGGAGGGATC
AACGTGACGGTGATAATGGACAGCTGGATCTCATGTCAGATACCATGGGTCAAGGGCCTG
GGTGCAGAACACTGAAGTGGCAGAACTGCCCTAAATTCTAGTCAGCTGAAGTGGAGGCCCTG
ACAGTGCACCTAAATCTTGGAACATCTGCTTGTCAAGTCTTACAAGAACCTTGTCTTC
TACTGGATTCTGAAAGCTGGTCATATGGTCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGACAGAGGATAAAATCATTTGAT
GGAGGCAATTGGAAATTATTTCTGCTCTTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPPLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTFGSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWSPVDSVLSSWGPYLVSMSLLEDGLAEVSKVAEQVILNAVNKGLYRE
ATELGWKAEMIIIEQNNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCGCTC
GGGCTGGACTCAGGAAGCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGAGAGGACGCCAACTCGGGCGTTGGCGTGGCA
GGGGAGGCCGCGCTGTGGGATTCCCACGGTATGCGGAGTGAGCCCTGCTCAGGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCTCTGGAGCCCTGCAGGCCACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTCAACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGCAACCTACACTAAACACATCCAGGCCATCTGCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAAGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGGGAGGATGCCCTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGGCCACACTTGTAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCTGGCCACTACTCTTTTCCCTCT
TCTCTGGCTCTCCACTCTGGGCCGGTCTTGAGCCTACCTGAGCCATGCGCCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTCTGCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLARAGLRLRKPEQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSSLHRWALTAACFETYSSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCVTGWGYIKEDEALP
SPHTLQEVLQVIAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHVVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVITGTVGLHVGTPSVIRKRYNLTSQDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDEDLSAYIQRNTTELMAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPLITNEIVDYISGGGSNVFPRPSYQEEAVTKFLSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTTRGCHESDLDEEVEVGQGFCSGPWGDPVTGWGTPSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCGGCGCCACACCTGTCAGCGGGCGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGAACAGTGCCTGGCATGGCAGGGATTCCAGGGCTCTCTTCTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTG
GCCATCCCGCTCCCTGCTGCTTGGCCAGTCTACCCCTCAATTAGCCAAGGCAGACT
TGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTCTAAGGGAACT
CCACTGCCACTTACGAAGAGGCCAGCAATATCTGTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGCAGATTATGGCTATGACAGC
AGGTTCAGCATTTGGAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGCAGAGAACATGCTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCTAAAGGCC
AAGTTAAAGATGGTGGTCAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGTGAACGCACCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACCTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGGCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCCTACACAGCAATGCGATGCCAGCCAGGGGGCAGGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTTCAGG
GCACCACTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAATCACTC
CTCTCAAAATGCCAGATTGCTATTGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTCTGGCAGCAATTAGGGCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCACTGGCGTGCACACGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAAGTG
GTTTGTGTATCATATCATATATCATTAAGCAGTTGAAGGCATACTTGCATAGAAATAA
AAAAAAACTGATTTGGGCAATGAGGAATTGACAATTAGTTAATCTTCACTGGCATA
CAAACCTTGATTTTATTCATCTGAACCTGTTCAAGGATTATATAATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKP
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTELQVGIYILSSSGDGAQHRD
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL
TQKLRVGFALKPKFDGGRGANDSTSAMP
EQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKPKHCRKFMKIGVSPPAKQLPGGRIHFGYDNDRPGNLVYRFCDVKDETYD
QQCDAQPGASGSGVYVRMWKRQQKWERKIIIGIFSGH
HQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGTCTCTCGAGCCTGCTGCCCTGCTCCCCGCCACAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGGAGGACACGACTGACACCCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAAATGGGACCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GCCCTGGCAGCTGGGAACCTGGCTCGGTCCCAGAAGGTGGGTGTTGCCCTGGGTGGAGC
CCCACCTGTGATTCTCTGGAAGGAAGGTGCTGTGAGACATTGCCCTGGTGCTCTGAG
CGCTCCATACAGTCTCAGAGCGGGCTCTGCCCATCTGCCAACCTGATGCCCTATACCC
CCCTCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTG
CCCACCTCAGACCCCTGCAAGACTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCGGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGCAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTCGGCACCCCTCCTGGGTGGAGAAGATCGTCAAGGGGTGCA
GCTCCGCGGGCGCCTCAGGGCGCAGCGGGACCGGGGCTGGATCTGAAAGGCGGCCAGATCCACA
CCGCGCCTCTAGGGCGCAGCGGGACCGGGGCTGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCCGGGGCTCGGGCGTTTCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCCAGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GCCCTCAGGCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCGGCCCCGCCCCGGGGCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTGTAAACCTGCCACATATCTTATTATGCCCAATTCAATAAATTATTTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MMVSGAPPALGGGCLGTFSSLSSATAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTTSRWVITAAHCFKDNLNKPYLFVSVLLGAWQLGNPGSRSQKVGV
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCACCAATGCACGGCTCCTGCAGTTCCGTATGCTTCTGCTGCCGACTGCTA
CTGCTGGTGGCCACCACAGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTGATGGT
GGAGCTGACAACCTCTACCGGGCCAGGTATCCCCGAGGCCTACAGACATGCTGCACATGA
GATGGGACAGGGAGCTGGCGCGCTTCGCCAACGGCTAACCGACGGCAGTGCCTGCTGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGCCATGGAGGAGTGGCACCACCGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGGCCAGGCCAGATGTGCGGCCACTACACGAGGTGATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAACGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGACTC
CGTGCCTCCAAATGTCCCTCGCTTACACTGCAAGAACCTCTGTGAACCCATCGGAAGC
CCGGAAAGATGCTCAGGATTGCTTACCTGTAACGTGAGGCCCATCTTCCGGGCACTGA
AGCATCAGACTCTAGAAAATGGGTACTCTTCTTCCCTAGCAACGGGATTCCGGTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGTTGGAAACCCAGGCC
CCAACCTCCTAGCAACGAAAGACCCGCCCTCATGGCAACAGAGGCTCCACCTTGCCTA
AACTGAGGCTCCCTTCATTTGGCAGCTCACAGCCTGCCCTCCITGGATGAGGAGCCAGTTA
CTCTCCCAAATGACCCATGTCCATATCCAAAATCAGCAGAACAGTGAACAGACAAAACA
AAAGTGCCTCTAGGAGGCCAGAGAAACTCTGGAACCCAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCTCAGTTTCCAGGCCAGGACAAGGCCAGGTGAGCTGCCAGGCCACACTGGAC
CACACGGGGCACACCTCTCCAAGTCCCTGCCCAATTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTCTGGCTGAGCTGCTCCCTGCCAGGTGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGGCCCTGGTATGTGTGGGGCCCTCTCTGGG
CTACTGCTCTGCCCTCTGGTGTGGCTGAATCTTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCACTGTCCTCTGTATCTTCCCCACCTGTCCCCAGGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAGGGAAAGGGTACGGGCATGTGCCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCCTGGCTGGCTGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCTGCCCTCCCTCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCT
CACTGCCCTACCTGGCTGGGCTGTGCCCCACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGGATTCCTAGGGCAGATGAAGGACAAGGCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGAGGGAAAGTAACCTCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFMLLLPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGRPYQECTPCSQC
PSGYHKNSLCEPIGSPEAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPVCITTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAAELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAECPDKPSVV
SGLNSGPSPGHVWGPPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

FIGURE 102

MVDVLLFLSCLLFHISRPDLSHNRLSF1KASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQLTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANLTLLVLKLNRRNRI8AIPPKMFKLQLQHLELNRNKIKNVGDLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMIEILQLDHNNLTETIKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDDLTFNHLSRLDDSSFLGLSLLNLTIHIGNNRVSYIACAFRGLSSLKTLSDLKNNE
ISWTIEDMNGAFSGDLKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLOQGNAFSQ
MKKLLQQQLHLLNTSSLLCDCQKLWLQWVAAENNFSFVNACAHPOQLKGGRSIFAVSPDGFVCD
DFPPKPKQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLRLEVFASEGGKYQCVISNHFGSSYSVAKAKLTVNMLFSTKTPMDLTIRAGA
MARLECAAVGHGPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVVKIEDIGVSYCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVKGETAVLQCAGGSPPKLNWTKDDSPLVVTER
HFFAAQGNLLIIIVDSVDSADGKYTCMNSTLGTERGVNLRSVIPTPTCDSPQMTPASLDDDG
WATVGVIIIAVVCCVVGTSLVVVIIYHTRRRNEDCSITNTDETNLPADIPSYLSQGTTLAD
RQDGYVSESEGSHHQFVTSSGAGFPFLPQHDSSGTCHIDNSSEADVEAATDLCFLCPFLGSTGP
MYLKGNVYGSDFPETYHTGPMRDPRTVLMDHYEPSYIHKKECYPCHPSEESCRSFSNISW
PSHVRKLLNTTSYHNEGPGMKNLCLNKSSLDFSNAPEPAVSSNSFMGTGKALRPHLDA
YSSFGQPSCDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

FIGURE 104

MLNKM TLHPQQIMIGPRFNRALFDPLLVLLALQQLVVAGLVR AQTCPSCSNSQFSKVIC
VRKNLREVPDGI STNTRLLNLHENQIQI KVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELF DNRLLTIPNGAFVYLSKLKE LWRNNPIESIPS YAFNRI PSLRRLDLGELKRLS
YISEGAFEGLSNL RLYLNLMCNLREIPNLTPLIKLDELLSGNHL SAIRPGSFQGLMHLQKL
WMIQS QI QVIERN AFNDNLQSLV EINLAHNNLTL PHDLFTPLHHLERIHLHHNPWCNC DIL
WLSWWI KDMAPS NTACC AR CNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLN VTEGMAAE
LKCRAS TSLTSV SWITP NGTVMTHGAYKVR IA VLS DGT LNFTN VTV QDTGMYTCMV SNS VGN
TTASATL NVTA ATTTPF SYFSTV T VETMEPSQDEA RTDNNVGPTPV DWETTN VTTSL TPQ
STRSTEKTFTI PVTD INSG IPI GIDE VMKTTKIIIGCFV AITLMAAVMLVIFYKMRQHH RQN
HHAPTRTVEI INV DDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIR MN SKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRELQPGSVAERPCPTTCRLGLDLLCSR
KRLARLFPEPLPSWVARDLDSHNRSLFIKASSMSHLQSREVTKLNNELETI PNLGPVSANIT
LLSLGAGNREVEIILPFLKEFQSLTLDLSSNNISELQTAFPALQLKYLTLNSNRNTSMPEGY
FDNLANTLVLKLNRNRISAIKPFKMFKLPOLOHLELRNRKINKVNDGLTFQLGALKSLKMOR
NGVTKLMMDGAFWGLSNMELIQLDHNLLTEITKGWLGYLLMLQBLHLSQNAINRISPDAWEFC
QKLSEELDTFNHLSRLDDDSFLGLLSSLNTLHIGGNRRSYIADCAFGRLLSLKTLDLKNEIES
WTIEDMGAFGASLKLRLRLIQLQNRIRSTIKKATAFTGLDNLBDLSDNAIMSLQGNQFSQMK
KLQQLHLNTSSLCDCLQKLWPQWAEENNFSQSFVNASCAPQQLKGRSIFAVSPDGFVCDDF
PKPKQITVQPETQSAIKGSNLFSICSAASSSDSPMTFAWKKDNELHDAEMENYAHLRAGGE
VMEYTTILRORSEVAIFQCVISNHFGSSYVKACLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAQPAQIAWQDKGGTFDPAARERMMHVMPEDDVFV1FDVKD1EIGVYCTAQNSA
GSISANATLTVLETSPSLRPLLDRRTVKGETAVLQCIAGGSPPPKLNWTKDSPPLVVTERHF
FAAGNGQLLIIVDSDVSADGAKYCTCEMSNSTLGTERTGNVRSLVTPFTCDSQPMATPSLDDDGWA
TVGVVIIAVCCVVGTSLSWWVIYHTRRRNEDCSITNTDETNLPADIPSYSLSSQGTJLADRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAATDLFLCPFLGSTGPMY
LKGNNVYGSDFETYHTGCSPPDRTVLMDHYEPSYI1KKECYPCHSEESERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCKLNSSLDSFANSPEPASVASSNSFMGTFGKA1RPHLDAYS
SFGQPSDCQPRAFYKLKAHSPPDLSGSSEEDGKERTDQEENHFTCQTOLNEYTRPNFQHLDAYS

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site

N-glycosylation site: amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020.

Glycosaminoglycan attachment site

Glycosaminoglycan and amino acids 886-889

Casein kinase II phosphorylation sites

Casein kinase II phosphorylation site.
amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site

tyrosine kinase p65 amino acids 663-675

N-myristylation site

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 682-687, 774-780, 822-828

Louise zipper pattern

Lysine zipper pattern.
amino acids 58-88 155-177

FIGURE 107

FIGURE 108

MEGEEAEQPWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFQAEEEPVVLVLSPEEPGPGPAAVSCP RD CACS QEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNR L TS RGLPEKA FEHL TNLYL ANN K
LT LA PRFLP NALIS D FA ANY LT KIY GLT FGQ K PNL RS VY LHNN K LAD AGL PDN M FNG SS NV
EV LIL SSN FLR HVP KHL P A LY KL HL K NN K LE K I PP GAF SEL S L RE LY L QNN YLT DE GLDN
ET FW K LSS LE Y LD LSS NN L SRV PAGL P RSL V LL H L E K N A I R S V D A N V L T P I R S L E Y L L H S N
QL REQ GI HPLA F QGL K RL H T V HLY NNA L E R V P S G L P R R V R T L M I L H N Q I T G I G R E D FATT Y F
LE EL NL S Y N R I T S P Q V H R D A F R K L R L L R S L D L S G N R L H T L P P G L P R N V H V L K V R N E L A A L A
RG A L A G M A Q L R E LY L T S N R L R S R A L G P R A W D L A H L Q I L D I A G N Q L T E I P E G L P E S L E Y L Y L
QNN K I S A V P A N A F D S T P N L K G I F L R F N K L A V G S V V D S A F R R L K H L Q V L D I E G N L E F G D I S K D
RG RL G K E K E E E E E E E E E E E E E TR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGACCTGCTCGGGCCCGGCCCTCGCCGCTGTCTCCGGAGGGCAG
CAGTAGCCGGGGCGGGAGGGCTGGGGTCTCTCGAGACTCTCAGAGGGGCCCTCCCATCGCGCCACCAACC
CAACCTGATTCCTCGGCTCTACCTGCAGGGCGGCCAGGGCTGCCAACATGGAAATTCTCTGGGGCTGGT
CTCTGGTATCTCTCGCTCTACCTGCAGGGCGGCCAGGGCTGCCAACATGGAAATTCTCTGGGGCTGGT
TGCGGCTATGTGTTATGGTGGGAGGATTGACTCTGCTGTGGGCTGGGCTGCCAGTCTTGGGGACAGTGTGCC
TGTGTCGGCAACCCAGATCCAAAATCATGCTGAATCTCGGGCAAACAGTGTCAAGTGTCACTCTGGTTATGCTGG
AAAAACCTGTATAAAGATCTAAATGAGITGCGCTGAAGGCCGGCCCTGAAGCACAGGTGATGAACACTTA
CGCGAGCTACAAGTCTACTCTGCTACAGGATAATGCTCATGCCGGATGGTTCTCTGCTCAAGTGCCTGACCTG
CTCCATGGCAACACTGCTAGTATGGCTGTGATGTGTTAAAGGACAATACCGTGCAGTGCCTCATCCCTGGGCT
GCCACCTGGCTCTGTAGGGAGGACTGTGATGATGTGCTCAAGGAAGGCCCTCTGCCCTAGGATT
TAGGAATGTGTCACACTTGGAGGACTACATCTGCAAGTGTCAAAAGGCTTCGATCTCATGTATATTGGGAGG
CAAATATCAATGTGATGACATAGACAGAATGCTCACITGGTCAAGTATCAGTGCAGCAGCTTGTCTGATGTTATAA
CGTACGTTGGGCTACAGTGCATAAGNAGGATACCCAGGGTATGACTGACTCTGTTGTTATACTCCAAA
AGTATGATTGAACTTCTCAGGTCCTATTGATCTGAAAGGAAATGTCCTTAAAGGGTACACAGGAAA
TAATAATGGAATTCTCTGTGTTGGAGTACTTGTGCTGGCCCTCGGAAGACACCATATACTCTCTCATCTACCAAA
CAGGCCACTCTTAAGCCAAACAAAGACCTACACCCACTACACCCCCAGAAAGGCCAACACCCGACTGAACTATAGC
CTGCCAACAGAGCTCAGAACACCTCTACCCACTACACCCCCAGAAAGGCCAACACCCGACTGAACTATAGC
ACCAAGCTGCCAGTACACCCGAGGATTACAGTTGACAAACAGGCTACAGGACAGACGACCCCTCAGAAACCCAGG
AGATGTGTCAGTGTCTCGTACACAGTTGATCTTGGCATGACTTGTGGATGGTACAGGGAGAACAGACAA
TGACTGCACTGGAAACCATCAGGGGCCAGCAGGGTGGACATAATCTGCAAGTGTGCGCAGCCAAAGGCCAGG
GGGAAAATCTGCAACCTTGTGCTACCTCTGCCGCTCATGCTCAGGGGACCTGTGCTGTGATTCTCAGGCA
CAAGGTGACGGGGCTGCACCTCTGCCGACACTCCAGGTGTTGTGAGAAAACACAGGTGCCCACGGAGCACCCCTGTG
GGGAGAAAATCTGCACTGGGCTATGGGCAAGGAAACACAGATCACCTTGCGGAGGGCTGACATAGAGGCAATCACA
AAGATGTAAAGGGTTGGAAAAAAAGATCTGATGTTAAAGGAACTTAAAGGAACTGCGATTATTGACCTTGAGAAG
AGAAGACTGAGGGGAAACCATCTGATGTTTCTCAACTATGAGAAGGGTTGGCAGAGGAGGGTGGCAGACCTGTG
TTCTCCATATGCACTAGAAATGAAACAAGAGGAACTGGCTTAGACTAGACTATAAGGACCATTTCTGGCAGG
GCCATTGTTAGAATACTCTATAAAAAGAGTGTGAAAATCTCATGATCTCTCTCTTCTAAAAAAATTAGA
TAAAATTTGCTTATTTAAGATGTTAAAGATGTTCTACCCAGGAAAAGTAACAAATTATAGAATTCTCCAAA
AGATGTTTGTATCTACTAGTAGTATGCACTGAAACTTAAAGTCTTAAAGGAACTTAAAGGCTTAAATTAGG
CATTTCCCTCTGACCTCTTAATGGAGGGATTGAAAGGGGAAGGCCAACAAATGCTGAGGTCACTGAAATA
TCTCTCCCTTATGGCAACTCTAGCACTTAAAGGAAAGGAACTTAAAGGCTTAAAGGAACTTAAAGGAACTTAAAGGAA
AGATATTGTTAGTATCTCACTGTTCTAGTGTGCTGGGGTGTGTTCAATGTTCTCATGTTAAAGGTATAAGCC
TTCTATTTGTCATGGATGTTGAGTCTTCACTGATTTTTTAAGAGATCTTCAAGGAACACAGTGTAGAGAG
ATTTCATCGGGTCATCTCTCTCTCTGCTGTGACAGTTATCTGCTGCTGAGAAAGACTGCTGGCTGCC
ACACGGGCAACACCTTCTTCACTCAGTGTGATTGAGTTCTTCTTCTTATCAATTGGACTCTCCCAAGGTTCCAC
AGAACAGTAAATTTTTGAACTAAGGTACAAATGAGTAAAGGCTCTGCTCATTTAACCTGGTAAAGGCAAGGCTG
AGGGGGAAAATAATCAATTAGCCTTTGAGTAACGGCAGAAATATGCTGTAGATCTCCATTTTAATGTTTCTT
TCCATTATGGTCATAACTGTCACAGCTGAAGATGAAAGGGAAAATAATGAAATTCTTACTTTGATGTC
TGATACATTGCACTAAACTGTGAGGAAGATGTTCTCAAAGTACTGTATAACATCTGTTTATTATTAATGTTT
CTAAAATAAAAAAATGTTAGTGGTTCTCAAATGGCTATAAAAACAATTGTTAATTTGAAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCOPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCWKRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRCTVDVDECATGRASCPFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSGYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKDTGNNNWPDVGSTWWPKTPYIPIPITNRP
TSKPTTRPFPKPTPIPTPPPPPPLPTELRPLPPTPERPTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSLVHSNCNFHDHGLCGWIREDNDLHWEPIRDPAQQYLTVA
KAARLVLPLGRLMHSGDLCFLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGCTCAAGGTCTCACAACTTTCTTCTTGCACAGGTGCTGCTGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGCAGAGGTAGGCCCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGACATCAGACATGGCTATGGCTATTGGAGAGACCCA
CACAAATGCCAAATTAACCTACTGGGCTCTGTGAATAACTCTGTGGTCTGACTTGGAAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATGTGAAGGTCACACATTGAGGAATGGAACCTCTATCTGCCAGTC
GAAGGATACAAGTCACGGGTGATGATCCTGCAACAGGAGTGGTGCAGATTCACTCTCCCT
CTGGGGCTGGAGATGGGGAAACATGACCTGCACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGCCACACCAGCTCCACCTACTCTTTT
TCCCCAAACAACTACCCCTCATATTGCTTCAAGTAACCAAGGAACAGATTGGGAATTACAGCT
GCCTGGTGGAGGAACCCGTGCACTGAAATGGGAAAGTGTATCATTATGCCATCATATTATT
GGACCTTATGGACTTCAGTGAATTCTGTAAAGGGCTAAAGTAGGGGAAGTGTCTACTGT
TGACCTTGGAGAGGGCATCTATTGTGATGTTCTGCTGATTCTCATCCCCCAACACCTACT
CTCTGGATTAGGGAGGACTGACAATACATACATATTCAAGGATGGGCTTACACAAACATAAC
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGCTGTGCTTACACAAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCATTCCGTAGGACTGGGAGAGCTTGC
CACAGAAAGGAAAATATTGTCTACCTTCTAGAAGTATACTGGAAATATCACTATTGGATT
ATATCCATGTGCTTCTCTCTTCTATGGAAAAAAATATCAACCCCTACAAAGTTAAAAACAGAA
ACTAGAAAGGCCAGAAACAGAAACAGAAATCAGGAAAGCTCAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAAATATGAATTGTGCTTCTCAGATGTTCTGGTGTCTCCAGG
ATTCTCAAGCAGGTCTGGTCCAGCTCTGATTGTGATCTGGGCAAGATTGCAAGCTACAGT
GTATGGAAAGTTATTCAAGCACATCCCTGCCACAGCAAGGACATCCAGAGTGAACCTTCATGG
GCTAAACAGTACATTGAGTGAATTCTGAAGAAAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAAATCTGGAAATCAGTGAAGAAAACAGGACCAACACCTCTTACTCATTATTCTTACA
TGCAGAAATAGAGGCAATTATGCAAAATTGAACTGCAGGTTCTCAGCATATACAAATGTCTT
GTGCAACAGAAAACATGTGGGAAATTCTCTAGTGGAGACTGTTCTCATGCTGACGG
GGAGAACGAAAGTGCAGGGGTTCTCATAAAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCTACATCAACACACTGTGAGACTATCTGTCTACCTACAAA
TGTGGAAAACTTCTACATTGTGTCATTCTCAGCAGACTTTGTTTATTAAATTTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTCTTCAAAATTCTATCTTGTATTITGTACAA
CAAAGTAATAAGGATGGTTGCAACAAACAAAACACTATGCCCTCTCTTTTCAATCACC
AGTAGTATTGGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTITTA
TTTTTCTAAGGAAAGATGGATTCAAAATAATTCTGTTTGTCTTAAAGGAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLGSVNVKSVPDLEYQHKFTMMPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSAQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNTLTCHVEGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEIDIGNYCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVEVFTV
DLGEAIIIFDCSADSHPPNTYSWIRRTDNTYIIKHGPRLLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSIRPSRSPVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCCCTCCGGAGTCCTGCAGTCCCCCTGGAGTCCTGGTGTGTT
GCTTTGGGTGCTCCCTGGACGACGGGGCGGAGCAACGTTCGCTCATCACGAGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAAGAATTATGCCCGTGGTCCCTGCT
TGTCAAATCTCAACGGGAATGGGAAAGTTTGCTGAATGGGAGAAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCGGACTGAGTGGACGTTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTAATTAGGGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTTATAAGTGTATAAGAGTGGAGAAGATATTGAGCCGTTTATCAG
GTTGGTCCAGGTTCTGATGAGTAGTGTCACTCTTCAGCTATCTATGTGGA
TCAGGACGTCGCAACTACTACTTTAGAACGACTGGTATTGCCAGTGTGGGAGCATATACT
GTTTTGCTTAGCAACTCTGTTTCCGACTGTTAGGACTCTGTATGATATTGTGGC
AGATTGCTTTGCTTCAAAAGCGCAGACACGCCATACCCATACCCCTTAAAAAAAT
TATTATCAGAATCTGCACACCTTGGTAAAAAGTGAGGAGGAAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGGCTGAAAGTAAAGAGGAAACAACAAAGACTTCCACAGAAATGC
CATAAAGACAAACGCTCTGGTCCATCATTGGCACAGATAAAATCCTAGTTAAATTATAG
TTATCTTAAATTATGTTGATAAAAACAGAAGATGATCATTGGTTGGTTGAAGTG
AACTGTAATTGGTCAATTGAGGGTCACTGAGTAGTGTCAATTAAATTGAAGAGTCTA
CATTAGAACATAAAAGCACTAGGTATAACAGTTGAAATATGATTTAACAGTATGATG
GTTTAAATAGTCTTAATTGGAAACATGGCAAGAACAGATTATGTTGATT
TTAATAAAACCTATTCTCAAGTCTGAGTTGGAAACATTACATTCCAAAGTATTGCTT
TGAGGTATTAAAGAAGATTGGAGGAAACATTCTCATTTGATATAATTCTCTG
TTCACTGTGTGAAAAAAAGAAGATATTCCATAAATGGAGTTGCCATTGCTCAAG
AAATGTTGTTTCACTGAGCAATTCTGTCATTAGGGTATATTCCAAAATTCTCTGT
ATTTTTAGGTATGCAACTAATAAAACACTTCTTACATTAATTAAATTACAGTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAAGTTCATGGTATTCTCTGATT
CAACAAAGTTGATTCTCTTGTATTCTTCACTACTATGGGTTACATTTTTATT
CAAATTGGAGATAATTCTGGAACATTGGTATTGGAGGAAACATTCTGTT
GTTTCAACTGAGTTACTGAGAGATCATCAAATTGAAACAATTCTGTAAATTAAA
TTGGCCACTTTTACAGATTACATCATTGCTGAACCTCAACTGAAATTGTTTT
TTCTTTTGATGTAAGGTGAACATTCTGATTGGTCTGATGTGAAAAAGCCTGGTA
TTTACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCAATTCTACTCAGGAAAAAG
CATCTCTGTATATGTTAAATGTTGCTCATATAACAGAAAGTTCTAATTGAT
TTACAGTCTGTAATGCTGATGTTAAAATAAAACATTTTTATATTAAAAGACAA
ACTTCATATTATCCTGTTCTTCTGACTGGTAATATTGTTGAGATTTCACAGTAAA
GTCAGTAGGATGGAACATTAGTGTATTCTTACTCTTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGAAATCATAAAACAAATGAACACTGACCCATTACGTAGTAGAC
AATTCTGTAAATGTCCTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATGTAATATAACAGTTCTTAAAGCCCTCTCCTTAAAGAATTAAATATTGAC
AAAGAGTTGGATGTTGAACTTGTGATGCCCTAGAAAAATATCCTAACGACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWPGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GGCAGTGTCCAGCTGGGAGACCGTGTATAATTGTTAACATAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCCCAAGCAGTGTCTAACCAGTGGACAGGGGATTGGAAGAGCGGG
AAGGTCTGCCAGAGCAGTGTGACACTTCCCTCTGTGACC**ATGAA**ACTCTGGGTGCTGC
ATTGCTGATGCCCTGGTTGGTGTCTGAGCTGTGACGGCCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATCAGAGAAGAGCTGGTCACTGTGAATGCCAACAACTGG
CTTGTGGAGAAGCCAAGCTTCAAGATTAAAGAGCTGGCCAAAAATGGAAGCCGTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGTCAACCTGTGAATGCCAACAACTGG
TGAAGCGGCTAAACACAGATGGCTGGCTGGAGGACCTTGCTCTGAGGACTCAGCTGCA
GTTTTATGCCAACCTCTGTGACAGGGCAGTTCTCCCACGTATGAGGAGAGATAGG
AGCTGCCAACGCCCCGTATGAGACTTCAGGACACATAACAGGCTGGACCCAGGCACAAATTCCA
GAGGGGAACTTCCAGGAACCAAGTACACAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCAACATGAAGGGACTATTATCATACGGTTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGGGCCAACACAACAACTCACAGGTGCTGACTACCTCA
GCTATGCTCTTCCAGTGGGTGATCTGCACCGTGCCTGGAGCTACCCGCCGCTGCTC
TCCCTGACCAACGACCAACAGCTGGAGGAAATCTGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTGACAACCCAGAGGCA
TCTATGAGAGGCCCTGGACTACCTGCTGAGAGGGATGTTACGAGAGCCTCTGCTGGG
GAGGGTGTCAAACGTACACACCCCGTAGACAGAAGAGGCTTTCTGTAGGTACCCATGGCAA
CAGGGGCCACAGCTGTCATTGCCCCCTTAACAGAGGAGGAGCAGTGGGACAGCCGACAA
TCGTCAAGTACTACAGATGTCATGTCATGAGGAAATCGAGAGGATCAAGGAGATCCAAA
CTTAAACTGACGAGCCCCGCTGTGATCCAAAGACAGGAGTCCACTGTCGCCAGCTA
CGGGGTTTCAAAGCTCTGGCTAGAGGAAGATGACCCCTGTTGAGCAGTAAATC
GTCGGATGCGCATATCACAGGGTTAACAGTAAGACTGCAAGAAATTGTTACAGGTTCAAATC
TATGGAGTGGGAGGACAGTATGAAACCGCACTTCGACTTCTCTAGGGCACCTTGTGACAGCGG
CCTAACAAACAGGGGAATAGGTTAGCGACGTTCTTAACATACATGAGTGTAGAAGCTG
GTGGTGGCCACCGTCTCCCTGATCTGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGGGACCCGGAAAGGTGACTACCGAACAGCATGCTGCC
TGTGCTTGTGGCTGCAAGTGGCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGATTGACT**TGAC**ATCCTTTCTGCTCTCCCTTCTGGTC
CTTCAGGGCATGTCACCTGACAGCACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCTGT
GTGACTGAAGTCCCGAGCCCTTCCATTCAAGCTGTGCCATCCCTGGCCCCAAGGTAGATCA
AAGTGGCTCAGCAGAGTTAGCTGTCTAGCGCTTACCAAGGTGCCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCTAGTGAACCAAAGTCTGTACCTTGTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAATAAAATGTCCCTACAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGLAHPVNAYKLVKRLNTDWPALELDLVLQDSAAGFIANLSVORQFFF
TDEDEIGAAKALMRLQDPTYRLDPGTISRGEGLPGTKYQAMLSVDDCFGMGRSAYNEGYYHTV
LWMEQVLKQLDAGEEATTTKSQVLVDLYSYAVFOLGDLHRAELTRRLLSLDPSSHERRAGGNLR
YFEQLLBEEEREKTLTNQTEAEELATPEGIYERPVDYLPRDVTYESLICRGEGVKLTPRRQKRLF
CRYHHGNRAPQOLLIAFPKEEDEWDSPHIVRYYDVMDSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTENRNLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAFWYNLLRSGEQDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCCTCTTCTTTAGTGGAAAGACAGACATAATCCAGTGAGTGAAATTGATTGT
TCATTTATTAACCGTTTGGCTGGGGTTAGTTCGCACACCTTCAGTTGAAGAGCAGGAGAAGGAGTTGTGA
AGACAGGAAACATCTCTTCTGGGGTAGCTGGTCTGGAGGGGCCCTCTGGCTCTGGCTCATGTACGCC
CAGGTTCTCTGGTTAACACTGAAGGACTACTAGGCTCTGGCCCATCAATTGATCTTGAGGTGJGCC
CTGGGGCACCACTGGCAGGGCTACACCAATGGACTGAGCTCCCTTGTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGAGGGAGGAGGAGGAGGAGGAGAAGAACTCAGATTGAGCTCGGCTAGACAAAGTG
ATGAAAGACTTCAACACCCCGGATTGGGCTCTGGCTCCCTGAGGGCTGTCTGGCTCTGACCTCCGGAGCTAC
GGTACATCAGACAGAGCTGGCTCCCTGAGGGCTGTCTGGCTCTGACCTCCGGAGCTACACTGTCCA
CTTGCGCTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTGGCTACTTCACTGGCAGGGGGGG
CCCGCGCTGGAGGGATGAGCGAGGAGTGGGGATGAGCGGGCTGGCTCATGGCTCATGAGAGACCTG
GCCACCTTCACACACACTTGGGGCAGACTACAGCTGGCTCTCATGAGATGAGACACATATGCGAGGCC
CCCGCCATCTGGCAGGCCCTCTGGCCACCTCAGCATCACCAAGACCTGACTTGGCCGGAGGGAGGAGTTCATTG
GGCAGGGAGACAGGGCCGGTACTCTGATGGGCTTGGCTACCTTGTGAGGACTCTCTGCTGTGCTGC
GCCACATCTGGATGGCTCCGGAGGAGACATTCTCAGTGGCCCTCTGAGCAGTGCTGGACGCTGCCATTG
ACTCTCTGGGCTGGCGTGTCTACAGCAGGGGGAGCAGAGTACGGCTGGCTCATTTGAAGTGGGCAAATAGGG
ACCCGCTCAAGAGGAGGAGGAGCTGGCTTCTGAGTGGGGCTGGGCTACAGTGAAGAACACTCGAGGCTCAGA
ACCCGCTCCACACTGGCTGTGACCCCCGAAGGGGGAGCAGGGCTGAGCTGGCCCTTGGCTCTGCTCTTCA
CACCAACACTCTGGTTGAGGTGCTGGGACTACTTCACAGACAGCACCTTCTCTGTCAGATGGG
CTCCCAAGTGGCCACTAGGGGCTGAGGGGGCTGAGGGGGCTGGGTAGTGGCTGGAGACTGCCCTGGAGCAGCTGA
ATCGCGCTATGCCCGCCCTGGCTTCCAGAACAGCGGACTGCTCAACGGCTATCGCGCTTGCACCCAGCAC
GGGGCATGGACTACCCCTGGACCTGCTGGTGGAGATGACACAGCGTGGCAGGGGCCCTGGCTCGCA
GGGTGAGGCTCTGGGGCCACTGAGGGGGTGGAAATCTTATGCCCTATGCTGAGGACCCGGAGTGC
AGCTGGTCTGCCACTCTGGTGGCTGAAGCTGCTGAGGCTGGCTTCTGGAGGGCTTGGAGCAATGTCC
TGGAGCCACGGAAACATGCTACCTGCTACCCCTGTTGGTACGGGCTACGGCCCGGCTTCTGGAGGGCTTGGAGCAGTCCAG
ACCCATTCTTGGGGTGAAGGCTGAGCAGCGAGTTAGCGACGGTACCTGGAGGGCTGGCTGGCTCG
CTGTCAGGAGCAGAGGCCCCCTTCCAGGTGGACTCATGGACGTGGCTCTGAGAAGAGCACCCCTGTGGACACTCT
TCTCCCTTACCCACCTGAGGCAAGGCTGGCCGAAGTCTCTGCTTACACAGAGATCACCCCAGGGCCC
GGGGGCTGGCCCTGACCCCCCTCCCTCTGGTGTGACCCCTCCGGGGGCTCTATAGGGGGAGATTTG
ACCGCAGGCTTCTGGAGGGCTGCTCTACACAGCTGACTACCTGGGGCCGAGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGGCCCTGGAGGGCTGGAGGGTGAATGGATTTTCTCCGGGTTCTAGGGCTCC
ACCTCTTGGGGCGTAGAGCAGGGCTGTGGAGAGTTCTCTGGAGACTGCACCCACAGGCTCAGTGAG
AACTCTACCAACCCGGTGGCCCTCAAGAACACTGGAGGAGGCTAGGGGGCTGGGGCCGTGCCAGCTGGCTATGGCTCTTTG
AGCAGGGAGGCAAGGCAATAGCATTAGCCGGCTGGGGCCCTAACCTCATTTCTTGTGCTGCTCAGCC
CAAGAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSSRARLD
QSDEDFKPRIVPVYRDPNPKYKKVLRTTRYIQTTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRRLYFTGQRGARAPAGMQMVSQSHGDERPAWLMSETLRHLHHTFGADYDWFFIMQDDTY
VQAPRRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIQLQAQIRNLTVLTPEGEAGLSWPVGLPAFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPQLQGASRADVGDALETALEQLNRYYQPRRLRFQKQRLLNGYR
RFDPARGMETYLTDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPLLL
VAEAAAAPAFLEFAANVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKA AAAEELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKHPVDTLFFLTTWTRPGPEVLRNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPPGPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAALEGLEVMDVFLRSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQALMALFEQEQA ST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGGCACAACGTGAGAGGAACCCGTGCGCGCTGCGCTTCCTGCCCCAAGCC
GTTCTAGACGGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AACGATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTAACAGCTCTAACAAAGAAGATATCTTGAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTTGAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTTGGACAAACACTGTGACAAAGCAG
AGTTCTTCAGTTGAAATGTTAAAGTGTGAGTCATTAAATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACA
GTTCTTCCTGCACGCCCAACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGAAAGGAGGAATTGCTTAAGTGTAGAATCAATGAAAAGACTTAAACGCC
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCGAAATATGCTGGAGTATTGCGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAAGTAGAGGCTGTTCAAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCGATGTGATGATGATGGGTATACCGCCTTAGGGCATTGGGATATTTC
GATGCAATTGGTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGATAGGACGTGTGTCATTATTGTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGAAATG
TGTGGAAAGAAGTGTAAAGAATAATAATTGCAAATAACTATTAAATAATTAT
GTGATAATTCTAAATTGAAACATTAGAAATCTGTGGGGCACATATTGCTGATTGGTT
AAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTAATT
TGTGATTAAAGTAAACTTTAGCTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCAAGTCCAATGGATTGCTTCTCAAATGTACAACAGCAACTAAAGAAA
ATTAAAGTGAAGTGAAGAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIIIVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFIAIENKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDQQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHI FNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGCGTCGATCTTACCAACAAAACACTCCTGAGGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGTTCTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCCTAGTCAGTCAGCTACCTGAGAAATTCAACAGAGCTCTCCTGCT
CTTCAAACCTGTGATGAGAAAAAGTTCAAGCTACCTGAGAAATTCAACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGTCATTGAACGGAAATTTCATCC
AGCTGCTACTCTTTCTACTGACACCATTCCCTGGCGTTAACGTTAAAGAAACTGCTCAGC
CATGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTCTACAAGA
AACCTAAAATGAGAGAGTTTTATTGGACTGTCAGACCAAGGTTGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTTCTGGATGTAGGGGAGCCAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTCGGATTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAATCTTTAAGAACAGAACAGGACAACACTCAAATGTGAAAGGAAGAGCA
AGAACATGCCACACCCACCAGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATAACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAAA
AAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFILWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGGGSVKNCCPLNWEIFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQVWDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCGCCCTGCCGTGGCCCCCTCAGAACCCCTCGACATGGCGCTGAGGCCGCCACCGCGAC
TCCGGCTCGCGCTGGCTGACTCTCTCTCTGCTGTTCAAGGGCTGCCTGATAGGGCTGTAATC
TCAAACTTCCAGAACCCCGGGCTGAGAATTTCAGGAAGTTCAGGAACTGCTGCATCATTACGGATTCG
AGAACAGTGGCCAGGATCTAGTGAGAAGAAAATTCAAGATGAAACACCACATATGTGTTTTGACAACAAA
TTCAAGGAGACTTGGCGGTGCTGAGAAGAAAATCTGGGAAGACATCCCTGAGAAGATCTGAACACGGAGAG
ACTCTGGCAAGTGAAGCCAGTGACCCCTGCTGTAGACTGCCAGGGCTGACAGTAGGCAAGATGCCAACACTGC
ACTCTGGCAAGTGAAGCCAGTGACCCCTGCTGTAGACTGCCAGGGCTGACAGTAGGCAAGATGCCAACACTGC
CCAGAGCCATCCAGATTTCGAATCTCTTCTTCACTAACTGAAACAGGCACTTGTGGTGTCACTGCTG
TTCAAGGAGACTCTGGGAGTACTACTGCAATTGCTTCATRGAGCAGGCTCACCCAGGTGTGAGGAGCAGG
AGATGAGAAGTCTAGTGGCAATCTGGGAATATTAGGGGGGTTCTGTGCTTGTGACTCTGGCCCTGA
TCAGCTGGGCGATCTGTGTCATCACAGCTGGCATCTAACATAAAACAGGATGGAGAAAGTCAAAAGA
ACCCAGGAAACCAAGATGGAGTAACTACATCCGACTGACAGGAGGCCACTTCAAGACACAGTCACTGGT
TGATCTGAAGCCCGGGTGTGGCTGAGAGCCAGTGACCCCTGCTGTAGACTCATTCAGAAGCTTTCGTTTGGCAAAGTGACCA
GGCAGCGAGAGCTGATGCACTGCCAGAGCTAGACACTCATTCAGAAGCTTTCGTTTGGCAAAGTGACCA
CTACTCTCTTACTCTAAACAGCACATTCAGATGGGTCTCTAATCTGTTCTGCTGATTCGGCATGAGATTAGG
GGAGCGAAACTGGTGGCTCACTGAGTTGGGTCTCTAATCTGTTCTGCTGATTCGGCATGAGATTAGG
GTGATCTGAAGGAGTCTAGTGGCTCACTGAGTAAACGCCGGTCTGTGAGCAGGATGTTCAACACTGGCTT
CAGCAGGCCAGCACCACTGTGAGATGGCAGGGTGGCTGAGCACACAGGCCATCCGGCGGAAACCCA
GAAAAGGCTTCTACACAGCAGCTTACTCTCATGGCCCAACAGACACCACCGCAGITCTCTTCTAAAGGCTTGC
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ACCTCTCTTGGCTCAAGTGGAGTCTTGTGTTTATTTGATTATGAAAGAAAATTCTTAACTGTAAATATTGT
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CACACAGGTTTGGCTTCTTCAAGGGAACTCATCTGTCATCACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAAAATCCAGTTAGGAAATCTGAAATCAGTTGCTCATCTCTTCAAAAGAACCTTCAAGGTTAGGTTCAACT
GCCCTCTTCTGAGATGACTGGACAGCTGTCACCCAGAGGCCACCCAGAGCCTCAGATGTCATACACAGATG
CCAGCTGCTGGGGCCAGGGGGCCCTGGCAGTGGCTGTGCTCCAGTGGCTTACTCATGGCCCTTGTGTTCATCCAGCAGC
TCTCAGGGGGCACTGGAGGACACTGGTGTCTTCACTGAGCTCCAGCTTGGGCTCTGTAACAGACCTT
TTTGGGTTATGATGCTCACAATAGGGCCCCCAACTGCTATTTTTTAAAGTTGTTTAAAGGTTTAAAGGTT
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CCCACTGTTCTCTTGGCAAGGAAACCCAGGCAACCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GGAGTGGGGCCAGCTGGCCCTTAAAGAAGCTGAGGTGGAGCAGCAGGCTGGGAGAACCTGGGGGGAGAAAAG
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GCCGTGCTGGACTCAGGACTGAAGTGTCTGAAGCAGGAGCTGCTGAGAGGAGCACTTCACTGTTGCTGG
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CCTCCATCACTGCTCCCTGGTCAAGAGGGATGGCTCCCACCCCTCAGCTGGTCTGCTGCTGCTGCTGCT
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CGGAAAGGAAATACTGTGTTATTAAAGATGATGACTCAAGACTGGCCGATACAGGGCTGTGATTCT
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FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
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><MW: 35020, pI: 7.90, NX(S/T): 3
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EIDEIVIELTVQVKPVTCPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIAASNDGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGINCCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267